

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 11, 2004, 11:32:23 ; Search time 6027 Seconds
(without alignments)
10945.429 Million cell updates/sec

Title: US-09-807-949B-1
Perfect score: 1522
Sequence: 1 acagtcagcgcgatggctcc.....ttaaaataaattttataat 1522

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :					GenEmbl:				
1:	gb	ba:	*		1:	gb	ba:	*	
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5:	gb	ov:	*		5:	gb	ov:	*	
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27:	em	sts:	*		27:	em	sts:	*	
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29:	em	vi:	*		29:	em	vi:	*	
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32:	em	htg_other:	*		32:	em	htg_other:	*	
33:	em	htg_mus:	*		33:	em	htg_mus:	*	
34:	em	htg_pln:	*		34:	em	htg_pln:	*	
35:	em	htg_rod:	*		35:	em	htg_rod:	*	
36:	em	htg_mam:	*		36:	em	htg_mam:	*	
37:	em	htg_vrt:	*		37:	em	htg_vrt:	*	
38:	em	sy:	*		38:	em	sy:	*	
39:	em	htgo_hum:	*		39:	em	htgo_hum:	*	
40:	em	htgo_mus:	*		40:	em	htgo_mus:	*	
41:	em	htgo_other:	*		41:	em	htgo_other:	*	

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1522	100.0	1522	6	AR074439	Sequence AR074439
2	1522	100.0	1522	6	AR081119	Sequence AR081119
3	1522	100.0	1522	6	AR085316	Sequence AR085316
4	1522	100.0	1522	6	AR088064	Sequence AR088064
5	1522	100.0	1522	6	AR104223	Sequence AR104223
6	1522	100.0	1522	6	AR143487	Sequence AR143487
7	1522	100.0	1522	6	AR171392	Sequence AR171392
8	1522	100.0	1522	6	AR171563	Sequence AR171563
9	1522	100.0	1522	6	BD243152	MN gene a BD243152
10	1522	100.0	1552	6	AX330007	Sequence AX330007
11	1522	100.0	1552	6	AX332607	Sequence AX332607
12	1522	100.0	1552	6	AX333244	Sequence AX333244
13	1522	100.0	1552	6	AX336174	Sequence AX336174
14	1522	100.0	1552	9	HSMATUMN	Sequence HSMATUMN
15	1520.4	99.9	1639	9	BC014950	Homo sapi BC014950
16	1517.4	99.7	1519	9	HAJ10588	Homo sapi HAJ10588
17	1399	91.9	1399	6	AR095263	Sequence AR095263
18	759.2	49.9	1965	10	MMU245857	Mus muscu MMU245857
19	457.8	30.1	1671	10	AB086322	Mus muscu AB086322
20	414.4	27.2	6521	6	AX795690	Sequence AX795690
21	414.4	27.2	6521	6	AX822141	Sequence AX822141
22	414.4	27.2	6521	6	AX825781	Sequence AX825781
23	414.4	27.2	10898	6	AR074442	Sequence AR074442
24	414.4	27.2	10898	6	AR081122	Sequence AR081122
25	414.4	27.2	10898	6	AR085319	Sequence AR085319
26	414.4	27.2	10898	6	AR088067	Sequence AR088067
27	414.4	27.2	10898	6	AR104226	Sequence AR104226
28	414.4	27.2	10898	6	AR143490	Sequence AR143490
29	414.4	27.2	10898	6	AR171395	Sequence AR171395
30	414.4	27.2	10898	6	AR171566	Sequence AR171566
31	414.4	27.2	10898	6	BD243155	MN gene a BD243155
32	414.4	27.2	88328	9	AL357874	Human DNA AL357874
33	414.4	27.2	187856	9	AF334829	Homo sapi AF334829
34	413.4	27.2	415	6	AR074454	Sequence AR074454
35	413.4	27.2	415	6	AR081134	Sequence AR081134
36	413.4	27.2	415	6	AR085331	Sequence AR085331
37	413.4	27.2	415	6	AR088079	Sequence AR088079
38	413.4	27.2	415	6	AR104238	Sequence AR104238
39	413.4	27.2	415	6	AR143502	Sequence AR143502
40	413.4	27.2	445	6	AR171406	Sequence AR171406
41	413.4	27.2	445	6	AR171577	Sequence AR171577
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43	380.2	25.0	10898	9	HSMNCA9	Homo sapi HSMNCA9
44	303.8	20.0	408	6	AX198178	Sequence AX198178
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ALIGNMENTS

RESULT 1	AR074439	AR074439	1522 bp	DNA	linear	PAT 28-AUG-2000
LOCUS	Sequence 1	from patent US 5955075.				
DEFINITION	AR074439					
ACCESSION	AR074439					
VERSION	AR074439.1	GI:10001194				
KEYWORDS						
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 1522)					
AUTHORS	Zavada,J., Pastorekova,S. and Pastorek,J.					
TITLE	Method of inhibiting tumor growth using antibodies to MN protein					
JOURNAL	Patent: US 5955075-A 1 21-SEP-1999;					
FEATURES	Location/Qualifiers					

QY 121 CCCAGAGGTTGCCCGGATGAGGAGGATTCCCCCTTGGGAGGAGGCTTCTTGGGGAA 180
Db 121 CCCAGAGGTTGCCCGGATGAGGAGGATTCCCCCTTGGGAGGAGGCTTCTTGGGGAA 180
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QY 241 CCACCCGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCT 300
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RESULT 3
AR085316
LOCUS AR085316 1522 bp DNA linear PAT 01-SEP-2000
DEFINITION Sequence 1 from patent US 5981711.
ACCESSION AR085316
VERSION AR085316.1 GI:10012085
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1522)
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE MN-specific antibodies and hybridomas
JOURNAL Patent: US 5981711-A 1 09-NOV-1999;
FEATURES
source Location/Qualifiers
1..1522
/organism="unknown"
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ORIGIN
Query Match 100.0%; Score 1522; DB 6; Length 1522;
Best Local Similarity 100.0%; Pred. No.3.4e-311;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 361 |GAGGCTCCTGGAGATCCTCAAGAACCCCAAGATAATGCCACAGGGACAAAGAAGGGGAT 420

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RESULT 4

AR088064

LOCUS AR088064 1522 bp DNA linear PAT 07-SEP-2000

DEFINITION Sequence 1 from patent US 5989838.

ACCESSION AR088064

VERSION AR088064.1 GI:10014827

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 1522)

AUTHORS Zavada, J., Pastorekova, S. and Pastorek, J.

TITLE Immunological methods of detecting MN proteins and MN polypeptides

JOURNAL Patent: US 5989838-A 1 23-NOV-1999;

FEATURES Location/Qualifiers

source 1. 1522

/organism="unknown"

/mol_type="unassigned DNA"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 3.4e-311;

Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 ACAGTCAGCCGCATGGCTCCCCTGTGCCCCAGCCCCCTGGCTCCCTCTGTGATCCCGGCC 60

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Db 61 CCTGCTCCAGGCTCACTGTGCAACTGCTGTCTCACTGCTGCTTCTGATGCCTGTCCAT 120

Qy 121 CCCCAGAGGTTGCCCGGATGCAGGAGGATTCCTCCCTTGGGAGGAGGCTCTTCTGGGGAA 180

Db 121 CCCCAGAGGTTGCCCGGATGCAGGAGGATTCCTCCCTTGGGAGGAGGCTCTTCTGGGGAA 180

Qy 181 GATACCCACTGGCGGAGGAGGATCTGCCAGTGAAGAGGATTCACCCAGAGAGGAGAT 240

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Qy 241 CCACCCGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCT 300

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AR104223

LOCUS AR104223 1522 bp DNA linear PAT 14-FEB-2001

DEFINITION Sequence 1 from patent US 6093548.

ACCESSION AR104223

VERSION AR104223.1 GI:12816931

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 1522)

AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.

TITLE Detection and quantitation of MN-specific antibodies

JOURNAL Patent: US 6093548-A 1 25-JUL-2000;

FEATURES Location/Qualifiers

source 1. .1522

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Query Match 100.0%; Score 1522; DB 6; Length 1522;

Best Local Similarity 100.0%; Pred.No. 3.4e-311;

Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DEFINITION Sequence 1 from patent US 6204370.
ACCESSION AR143487
VERSION AR143487.1 GI:15104773
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1522)
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE MN gene and protein
JOURNAL Patent: US 6204370-A 1 20-MAR-2001;
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Query Match 100.0%; Score 1522; DB 6; Length 1522;
Best Local Similarity 100.0%; Pred. No. 3.4e-311;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DEFINITION Sequence 1 from patent US 6297041.
ACCESSION AR171392
VERSION AR171392.1 GI:17910342
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1522)
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE MN gene and protein
JOURNAL Patent: US 6297041-A 1 02-OCT-2001;
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ACCESSION	AR171563		
VERSION	AR171563.1	GI:17910513	
KEYWORDS			
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ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 1522)		
AUTHORS	Zavada,J., Pastorekova,S. and Pastorek,J.		
TITLE	MN gene and protein		
JOURNAL	Patent: US 6297051-A 1 02-OCT-2001;		
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Qy	361	GAGGCTCCTGGAGATCCTCAAGAAACCCAGATAATGCCAGACCAAGAGGGGAT	420
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DEFINITION	MN gene and protein.		
ACCESSION	BD243152		

KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,
Horrigan, S., Soppet, D.R. and Weaver, Z.
TITLE Cancer gene determination and therapeutic screening using signature
gene sets
JOURNAL Patent: WO 0194629-A 516 13-DEC-2001;
Avalon Pharmaceuticals (US)
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Best Local Similarity 100.0%; Pred. No. 3.4e-311;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 811 ACCGCCCTTTGCCAGAGTTGACGAGGCCCTTTGGGCGCCCCGGAGGCCCTGGCGTGTGGCC 870
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Db 871 GCCTTTCTGGAGGAGGCCCGGAAGAAACAGTGCCTATGAGCAGTTGCTGTCTCGCTTG 930
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Db 1531 TTTTAAAAATAAATATTATAAT 1552

RESULT 11
AX332607
LOCUS AX332607 1552 bp DNA linear PAT 09-JAN-2002
DEFINITION Sequence 3116 from Patent WO0194629.
ACCESSION AX332607
VERSION AX332607.1 GI:18123241
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,
Horrigan, S., Soppet, D.R. and Weaver, Z.
TITLE Cancer gene determination and therapeutic screening using signature
gene sets
JOURNAL Patent: WO 0194629-A 3116 13-DEC-2001;
Avalon Pharmaceuticals (US)

FEATURES
source Location/Qualifiers
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ORIGIN

Query Match 100.0%; Score 1522; DB 6; Length 1552;
Best Local Similarity 100.0%; Pred. No. 3.4e-311;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACAGTCAGCCGATGGCTCCCTGTGCCCCAGCCCCCTGGCTCCCTCTGTTGATCCCGGCC 60
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QY 181 GATGACCCACTGGCGGAGGAGGATCTACCTGGAGAGGAGATCTACCTGGAGAGGAGAT 240
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QY 421 GACCAGAGTCAATTGGCGCTATGGAGGCGACCCGCCCTGGCCCCGGGTGTCCCCAGCTGC 480
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QY 481 GCGGGCCGTTCCAGTCCCGGTGGATATCGCCCCCAGTCGCGCCCTTCTGCCCGGCC 540
DB 511 GCGGGCCGTTCCAGTCCCGGTGGATATCGCCCCCAGTCGCGCCCTTCTGCCCGGCC 570

QY 541 CTGCGCCCCCTGGAACCTCTGGGCTTCAGACTCCCGCCGCTCCAGAACTGCGCCTGCGC 600
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DB 931 GAAGAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCCAGGACTGGACATATCTGCACTC 990

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DB 1531 TTTTAAATAAAATATTTATAAT 1552

RESULT 12
AX333244
LOCUS AX333244 1552 bp DNA linear PAT 09-JAN-2002
DEFINITION Sequence 3753 from Patent WO0194629.
ACCESSION AX333244
VERSION AX333244.1 GI:18123878
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Young,P.E., Augustus,M., Carter,K.C., Ebner,R., Endress,G.,
Horrigan,S., Soppet,D.R. and Weaver,Z.
TITLE Cancer gene determination and therapeutic screening using signature
gene sets
JOURNAL Patent: WO 0194629-A 3753 13-DEC-2001;
Avalon Pharmaceuticals (US)
FEATURES Location/Qualifiers
source 1..1552
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ORIGIN

Query Match 100.0%; Score 1522; DB 6; Length 1552;
Best Local Similarity 100.0%; Pred. No. 3.4e-311;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACAGTCAGCCGATGGCTCCCTGTGCCCCAGCCCCCTGGCTCCCTCTGTTGATCCCGGCC 60

Db 31 ACAGTCAGCCGCATGGCTCCCTGTGCCCCAGCCCTGGCTCCCTCTGTGATCCCGGCC 90
Qy 61 CCTGCTCCAGGCCTCACTGTGCAACTGCTGTCACTGCTGCTCTCTGATGCCCTGTCCAT 120
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Db 331 GAAGTTAAGCCTAAATCAGAAGAAGAGGGCTCCCTGAAGTTAGAGGATCTACCTACTGTT 390
Qy 361 GAGGCTCTGGAGATCCTCAAGAACCCAGATAATGCCACAGGGACAAAGAGGGAT 420
Db 391 GAGGCTCTGGAGATCCTCAAGAACCCAGATAATGCCACAGGGACAAAGAGGGAT 450
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Db 1531 TTTTAAAAATAAATAATTATAAT 1552

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LOCUS AX336174 1552 bp DNA linear PAT 09-JAN-2002
DEFINITION Sequence 6683 from Patent WO0194629.
ACCESSION AX336174
VERSION AX336174.1 GI:18126893
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Young,P.E., Augustus,M., Carter,K.C., Ebner,R., Endress,G.,
Horrigan,S., Soppet,D.R. and Weaver,Z.
TITLE Cancer gene determination and therapeutic screening using signature
gene sets
JOURNAL Patent: WO 0194629-A 6683 13-DEC-2001;
Avalon Pharmaceuticals (US)
FEATURES
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 3.4e-311;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ACAGTCAGCCGCATGGCTCCCTGTGCCCCAGCCCTGGCTCCCTCTGTGATCCCGGCC 60
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Db 1531 TTTTAAATAAATAATTTATAAT 1552

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source

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X65839.1 GI:1000701
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1552)
Pastorek,J.
Direct Submission
Submitted (11-JUN-1992) J. Pastorek, Institute of Virology, Slovak
Academy of Sciences, Dubravska 9, 842 46 Bratislava, SLOVAK
REPUBLIC
revised by [3] MAT
2 (bases 1 to 1552)
Pastorek,J., Pastorekova,S., Callebaut,I., Mornon,J., Zelnik,V.,
Opavsky,R., Zatovicova,M., Liao,S., Portetelle,D., Stanbridge,E.J.,
Zavada,J. and Burny,A.
Cloning and characterization of MN, a human tumor-associated
protein with a domain homologous to carbonic anhydrase and a
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3 (bases 1 to 1552)
Pastorek,J.
Direct Submission
Submitted (19-JUL-1994) J. Pastorek, Institute of Virology, Slovak
Academy of Sciences, Dubravska 9, 842 46 Bratislava, SLOVAK
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4 (bases 1 to 1552)
Pastorek,J.
Direct Submission
Submitted (28-SEP-1995) J. Pastorek, Institute of Virology, Slovak
Academy of Sciences, Dubravska 9, 842 46 Bratislava, SLOVAK
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On Sep 29, 1995 this sequence version replaced gi:558593.
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Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

22388257

12477932

2 (bases 1 to 1639)

Strausberg,R.

Direct Submission

Submitted (01-OCT-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada

info@bcgsc.bc.ca

Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAL Plate: 34 Row: i Column: 18

This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 9955947.

FEATURES

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 11, 2004, 11:32:22 ; Search time 643 Seconds
(without alignments)
10055.610 Million cell updates/sec

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Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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7	1522	100.0	1522	6	ABL68346 Kidney ca
8	1522	100.0	1522	7	ACC72730 Human can
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	26	293	19.3	305	4	AA523827 Human ova
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XX AAT09186;

DT 25-MAR-2003 (revised)
DT 19-AUG-1996 (first entry)

XX MuTu putative oncogene MN cDNA.

XX MuTu; endogenous; cellular component; MN; HeLa cell; diagnosis;
KW lymphocytic choriomeningitis virus; LCMV; putative oncogene; treatment;
KW neoplastic; pre-neoplastic; disease; antisense therapy; antibody;
KW vaccine; vertebrate; immunisation; ss.

XX Homo sapiens.

XX Key Location/Qualifiers
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FT /*tag= a

XX WO9534650-A2.

XX 21-DEC-1995.

XX 15-JUN-1995; 95WO-US007628.

XX 15-JUN-1994; 94US-00260190.

XX 07-JUN-1995; 95US-00477504.

XX 07-JUN-1995; 95US-00481658.

XX 07-JUN-1995; 95US-00485049.

XX 07-JUN-1995; 95US-00485862.

XX 07-JUN-1995; 95US-00485863.

XX 07-JUN-1995; 95US-00486756.

XX 07-JUN-1995; 95US-00487077.

XX (CIBA) CIBA CORNING DIAGNOSTICS CORP.

XX (VIRO-) INST VIROLOGY.

XX Zavada J, Pastorekova S, Pastorek J;

XX WPI; 1996-049679/05.

XX P-PSDB; AAR88058.

PT MN gene, protein and nucleic acid fragments - used as primers and probes

PT in the detection of MN antigens and antibodies, and in the treatment of
PT (pre)neoplastic disease.
XX
PS Claim 1; Fig 1; 102pp; English.
XX
CC The present sequence is the full length MuTu endogenous cellular
CC component, MN, cDNA clone, which was isolated from lymphocytic
CC choriomeningitis virus (LCMV) infected HeLa cells. Persistent LCMV, the
CC exogenous MuTu transmissible agent (MX), infection increases the
CC expression level of the MN gene. MN is a putative oncogene, and can
CC therefore be used in the development of prods. for the diagnosis and
CC treatment of neoplastic (NP), or pre-NP diseases. NP diseases can be
CC treated using DNA antisense to MN transcribed mRNA, anti-MN protein
CC antibodies can be used for the diagnosis NP or pre-NP diseases and a
CC vaccine contg. immunogenic amounts of the MN protein can be used to
CC immunise a vertebrate against a NP disease associated with MN antigen
CC expression. (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ Sequence 1522 BP; 297 A; 458 C; 453 G; 314 T; 0 U; 0 Other;

Query Match 100.0%; Score 1522; DB 2; Length 1522;
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DB 1441 GGAGCCGGTAACGTGCTGCTGCTCATTATGCCACTTCTTTTAACTGCCAAGAAATT 1500
QY 1501 TTTTAAAAATAAATAATTATAAT 1522
DB 1501 TTTTAAAAATAAATAATTATAAT 1522

RESULT 2
AAA16540
ID AAA16540 standard; cDNA; 1522 BP.
XX
AC AAA16540;
XX
DT 16-JUN-2000 (first entry)
XX
DE Human MN protein encoding cDNA SEQ ID NO:1.
XX
KW Human; MN protein; MN gene; oncogene; carbonic anhydrase; tumour;
KW oncogenesis; diagnosis; neoplastic disease; cancer; carcinoma;
KW MN/CA IX isoenzyme; ds.
XX
OS Homo sapiens.
XX
PN US6027887-A.

XX 22-FEB-2000.
PD
XX
PF
XX
PR 24-JAN-1997; 97US-00787739.
PR 21-OCT-1992; 92US-00964589.
PR 30-DEC-1993; 93US-00177093.
PR 15-JUN-1994; 94US-00260190.
PR 07-JUN-1995; 95US-00477504.
PR 07-JUN-1995; 95US-00481658.
PR 07-JUN-1995; 95US-00485049.
PR 07-JUN-1995; 95US-00485862.
PR 07-JUN-1995; 95US-00485863.
PR 07-JUN-1995; 95US-00486756.
PR 07-JUN-1995; 95US-00487077.
XX
PA (SLSC-) SLOVAK ACAD SCI INST VIROLOGY.
XX
PI Pastorek J, Zavada J, Pastorekova S;
XX
DR WPI; 2000-194827/17.
XX P-PSDB; AAY53228.
PT Nucleic acid based assay for diagnosing a wide variety of
PT preneoplastic/neoplastic disease comprises screening for the presence of
PT abnormal MN gene expression in a vertebrate.
XX
PS Claim 1; Fig 1; 87pp; English.
XX
CC The present invention describes a method of screening for
CC preneoplastic/neoplastic disease. The method comprises: (1) determining
CC whether abnormal MN gene expression is present in a vertebrate; and (2)
CC if abnormal MN gene expression is determined to be present in the
CC vertebrate, determining that the vertebrate has a significant risk of
CC having preneoplastic/neoplastic disease. The MN gene is an oncogene and
CC encodes an MN protein (also referred to as MN/CA IX isoenzyme). The MN
CC protein is a tumour associated carbonic anhydrase isoenzyme. The method
CC is used for detecting a wide variety of preneoplastic/neoplastic diseases
CC in a vertebrate, preferably a human. The disease detected is mammary,
CC bladder, renal, urinary tract, ovarian, uterine, cervical, endometrial,
CC vaginal, vulval, prostate, liver, lung, skin, thyroid, pancreatic,
CC testicular, brain, head and neck, mesodermal, gallbladder, rectal,
CC duodenal, jejunal, ileal, gastric, pancreatic duct, liver duct, gastric
CC mucosa, gallbladder epithelium, small intestinal mucosa, colorectal
CC mucosa, pancreatic duct epithelium or liver duct epithelium
CC preneoplastic/neoplastic disease. AAL16540 to AAL16617 and AAY53228 to
CC AAY53245 represent sequences used in the exemplification of the present
CC invention
XX
SQ Sequence 1522 BP; 297 A; 458 C; 453 G; 314 T; 0 U; 0 Other;
Query Match 100.0%; Score 1522; DB 3; Length 1522;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACAGTCAGCCGATGGCTCCCTGTGCCCCAGCCCCCTGGCTCCCTCTGTTGATCCCGGCC 60
Db 1 ACAGTCAGCCGATGGCTCCCTGTGCCCCAGCCCCCTGGCTCCCTCTGTTGATCCCGGCC 60
QY 61 CCTGCTCCAGGCTCACTGTGCAACTGCTGTCTACTGTCTGTCTGTATGCCTGTCCAT 120
Db 61 CCTGCTCCAGGCTCACTGTGCAACTGCTGTCTACTGTCTGTCTGTATGCCTGTCCAT 120
QY 121 CCCAGAGGTTGCCCGGATGCAGGAGGATCCCCCTTGGGAGGAGGCTCTTCTGGGAA 180
Db 121 CCCAGAGGTTGCCCGGATGCAGGAGGATCCCCCTTGGGAGGAGGCTCTTCTGGGAA 180
QY 181 GATGACCCACTGGCGAGGAGGATCTGCCAGTGAAGAGGATTCACCCAGAGAGGAGAT 240
Db 181 GATGACCCACTGGCGAGGAGGATCTGCCAGTGAAGAGGATTCACCCAGAGAGGAGAT 240
QY 241 CCACCCGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCT 300
Db

Db 241 CCACCCGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCT 300
QY 301 GAAGTTAAGCCTAAATCAGAAGAAGAGGGCTCCCTGAAGTTAGAGGATCTACCTACTGTT 360
Db 301 GAAGTTAAGCCTAAATCAGAAGAAGAGGGCTCCCTGAAGTTAGAGGATCTACCTACTGTT 360
QY 361 GAGGCTCCTGGAGATCCTCAAGAACCCAGAAATAATGCCACAGGGACAAAGAAGGGAT 420
Db 361 GAGGCTCCTGGAGATCCTCAAGAACCCAGAAATAATGCCACAGGGACAAAGAAGGGAT 420
QY 421 GACCAGAGTCATTGGCGCTATGAGGGCGACCCCGCCCTGGCCCGGGTGTCCCCAGCCTGC 480
Db 421 GACCAGAGTCATTGGCGCTATGAGGGCGACCCCGCCCTGGCCCGGGTGTCCCCAGCCTGC 480
QY 481 GCGGGCCGCTTCCAGTCCCGCGTGGATATCCGCCCCCAAGTCCGCCCTTCTGCCCCGSCC 540
Db 481 GCGGGCCGCTTCCAGTCCCGCGTGGATATCCGCCCCCAAGTCCGCCCTTCTGCCCCGSCC 540
QY 541 CTGCGCCCCCTGGAACTCCTGGGCTTCCAGCTCCCGCCGCTCCAGAACTGGCCCTGCGC 600
Db 541 CTGCGCCCCCTGGAACTCCTGGGCTTCCAGCTCCCGCCGCTCCAGAACTGGCCCTGCGC 600
QY 601 AACAAATGSCACAGTGTGCAACTGACCTGCTCCCTCTCTGGGTAGAGATGGCTCTGGGTCC 660
Db 601 AACAAATGSCACAGTGTGCAACTGACCTGCTCCCTCTCTGGGTAGAGATGGCTCTGGGTCC 660
QY 661 GGGCGGAGTACCGGGCTCTGCAAGTGCATCTGCACTGGGGGGTGCAGGTCGTCGGGC 720
Db 661 GGGCGGAGTACCGGGCTCTGCAAGTGCATCTGCACTGGGGGGTGCAGGTCGTCGGGC 720
QY 721 TCGGAGCACACTGTGAAGGCCACCGTTTCCCTGCCGAGATCCACGTGTTTCACTCAGC 780
Db 721 TCGGAGCACACTGTGAAGGCCACCGTTTCCCTGCCGAGATCCACGTGTTTCACTCAGC 780
QY 781 ACCGCTTTGCCAGAGTTGACAGGCTTGGGGCGCCCGGGAGGCTGGCCGTTGTCCTG 840
Db 781 ACCGCTTTGCCAGAGTTGACAGGCTTGGGGCGCCCGGGAGGCTGGCCGTTGTCCTG 840
QY 841 GCCTTTCTGGAGGAGGGCCCGGAAGAAAACAGTGCCTATGAGCAGTTGCTGTCTGCTTG 900
Db 841 GCCTTTCTGGAGGAGGGCCCGGAAGAAAACAGTGCCTATGAGCAGTTGCTGTCTGCTTG 900
QY 901 GAAGAAATCGTGAAGAGGCTCAGAGACTCAGGTCACAGGACTGGACATATCTGCACTC 960
Db 901 GAAGAAATCGTGAAGAGGCTCAGAGACTCAGGTCACAGGACTGGACATATCTGCACTC 960
QY 961 CTGCCCTCTGACTTCAGCCGCTACTTCCAATATGAGGGGTCTCTGACTACACCGCCCTGT 1020
Db 961 CTGCCCTCTGACTTCAGCCGCTACTTCCAATATGAGGGGTCTCTGACTACACCGCCCTGT 1020
QY 1021 GCCCAGGGTGTCTATCTGGACTGTGTTTAAACCAGACAGTGTGCTGAGTGTAAAGCAGCTC 1080
Db 1021 GCCCAGGGTGTCTATCTGGACTGTGTTTAAACCAGACAGTGTGCTGAGTGTAAAGCAGCTC 1080
QY 1081 CACACCTCTCTGACACCCCTGTGGGGACCTGGTGACTCTCGGCTACAGCTGAACCTCCGA 1140
Db 1081 CACACCTCTCTGACACCCCTGTGGGGACCTGGTGACTCTCGGCTACAGCTGAACCTCCGA 1140
QY 1141 GCGACGCAAGCCTTGAATGGGAGTGAATGAGGCTCCTTCCCTGCTGGAGTGGACAGC 1200
Db 1141 GCGACGCAAGCCTTGAATGGGAGTGAATGAGGCTCCTTCCCTGCTGGAGTGGACAGC 1200
QY 1201 AGTCCTCGGCTGTGAGCCAGTCCAGTGAATTCCTGCTGGCTGTGTTGACATCCTA 1260
Db 1201 AGTCCTCGGCTGTGAGCCAGTCCAGTGAATTCCTGCTGGCTGTGTTGACATCCTA 1260
QY 1261 GCGCTGTTTGGCCTCCTTTTGTCTGTCCAGCGTCCGCTTCTGTGAGATGAGA 1320
Db 1261 GCGCTGTTTGGCCTCCTTTTGTCTGTCCAGCGTCCGCTTCTGTGAGATGAGA 1320
QY 1321 AGGCAGCACAGAAGGGGAACCAAGGGGGTGTGAGTACCGCCAGCAGAGGTAGCCGAG 1380
Db 1321 AGGCAGCACAGAAGGGGAACCAAGGGGGTGTGAGTACCGCCAGCAGAGGTAGCCGAG 1380

QY 1381 ACTGGAGCCTAGAGGCTGGATCTTTGGAGAATGTGAGAAAGCCAGCCAGAGGCATCTGAGGG 1440
Db ACTGGAGCCTAGAGGCTGGATCTTTGGAGAATGTGAGAAAGCCAGCCAGAGGCATCTGAGGG 1440
QY 1441 GGAGCCGGTAACCTGCTGCTGCTGCTCATTTATGACCACTTCTTTTAACTGCCAAGAAATT 1500
Db GGAGCCGGTAACCTGCTGCTGCTGCTCATTTATGACCACTTCTTTTAACTGCCAAGAAATT 1500
QY 1501 TTTTAAATAAATAATTATAAT 1522
Db TTTTAAATAAATAATTATAAT 1522

RESULT 3

AAA52459

ID AAA52459 standard; cDNA; 1522 BP.

XX AC AAA52459;

XX DT 25-SEP-2000 (first entry)

XX DE Human MN cDNA.

XX KW MN protein; tumour associated cell adhesion molecule; oncoprotein;
KW proteoglycan domain; PG domain; carbonic anhydrase; CA domain;
KW abnormal expression; neoplastic disease; cancer; gene therapy; ss.

XX OS Homo sapiens.

XX FT Key Location/Qualifiers

FT CDS 13..1392

FT /*tag= a

FT /product= "Human MN protein"

XX PN WO200024913-A2.

XX PD 04-MAY-2000.

XX PF 22-OCT-1999; 99WO-US024879.

XX PR 23-OCT-1998; 98US-00177776.

XX PR 23-OCT-1998; 98US-00178115.

XX PA (FARB) BAYER CORP.

XX PA (VIRO-) INST VIROLOGY.

XX PI Zavada J, Pastorekova S, Pastorek J;

XX DR WPI; 2000-350752/30.

XX DR P-PSDB; AAB03005.

XX PT A molecule which specifically binds to a site on MN protein (oncoprotein)
XX and prevents adhesion of vertebrate cells to the protein, useful for
XX treating preneoplastic or neoplastic diseases such as cancer.

XX PS Example 1; Fig 1A-C; 154pp; English.

XX CC The invention relates to the inhibition of cell adhesion mediated by the
XX MN oncoprotein (also known as the MN/CA IX isoenzyme or the MN/G250
XX protein). The MN protein is a tumour-associated adhesion molecule which
XX comprises a proteoglycan-like (PG) domain (AAB03017) which contains the
XX protein's binding site, and a carbonic anhydrase (CA) domain (AAB03018).
XX Abnormal expression of the MN protein is associated with tumorigenicity.
XX The invention encompasses molecules (e.g., proteins and peptides) which
XX which specifically bind to a site on the MN protein, thereby preventing
XX adhesion of vertebrate cells to the protein in a cell adhesion assay. It
XX also encompasses MN proteins or MN protein fragments which can be added
XX to the extracellular environment to prevent the adhesion of vertebrate
XX cells to each other. The invention also relates to the identification of
XX the binding site of the MN protein and to a method of identifying a site
XX on an MN protein to which cells adhere, comprising testing a series of
XX overlapping peptides from the protein in a cell adhesion assay. The

CC invention encompasses a vector comprising an expression control sequence
CC operatively linked to a nucleic acid encoding the variable domains of a
CC MN-specific antibody, where the domains are separated by a flexible
CC linker peptide (AAB03035) and the vector inhibits the growth of a
CC vertebrate preneoplastic or neoplastic cell that abnormally expresses MN
CC protein. The invention also encompasses a vector comprising a nucleic
CC acid encoding a cytotoxic protein or peptide operatively linked to the MN
CC gene promoter, which inhibits the growth of a vertebrate preneoplastic or
CC neoplastic cell. Also claimed is a repressor complex that binds to the MN
CC gene promoter (AAA52473). MN proteins and peptides, MN-binding proteins
CC and peptides, and expression vectors encoding such proteins and peptides
CC are useful for treating patients with preneoplastic or neoplastic disease
CC (e.g., cancers) associated with or characterised by abnormal MN
CC expression. The present sequence represents cDNA encoding the human MN
CC protein
XX
SQ Sequence 1522 BP; 297 A; 458 C; 453 G; 314 T; 0 U; 0 Other;

Query Match 100.0%; Score 1522; DB 3; Length 1522;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACAGTCAGCCGCATGGCTCCCTGTGCCCCCAGGCCCTGGCTCCCTCTGTGATCCCGGCC 60
Db ACAGTCAGCCGCATGGCTCCCTGTGCCCCCAGGCCCTGGCTCCCTCTGTGATCCCGGCC 60
QY 61 CCTGCTCCAGGCCCTCACTGTGCAACTGCTGCTGTCACTGCTGCTTCTGATGCCTGTCCAT 120
Db CCTGCTCCAGGCCCTCACTGTGCAACTGCTGCTGTCACTGCTGCTTCTGATGCCTGTCCAT 120
QY 121 CCCCAGAGGTTGCCCCCGGATGCAGGAGGATTTCCCCCTTGGGAGGAGGCTCTTCTGGGAA 180
Db CCCCAGAGGTTGCCCCCGGATGCAGGAGGATTTCCCCCTTGGGAGGAGGCTCTTCTGGGAA 180
QY 181 GATGACCCACTGGGCGAGGAGGATCTGCCCACTGAAGAGGATTCACCCAGAGAGGAGGAT 240
Db GATGACCCACTGGGCGAGGAGGATCTGCCCACTGAAGAGGATTCACCCAGAGAGGAGGAT 240
QY 241 CCACCCGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCT 300
Db CCACCCGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCT 300
QY 301 GAAGTTAAGCCTAAATCAGAAAGAGAGGGTCCCTGAAAGTTAGAGGATCTACCTACTGTT 360
Db GAAGTTAAGCCTAAATCAGAAAGAGAGGGTCCCTGAAAGTTAGAGGATCTACCTACTGTT 360
QY 361 GAGGCTCCTGGAGATCCTCAAGAACCCCAAGATAATGCCACAGGGACAAAGAGGGAT 420
Db GAGGCTCCTGGAGATCCTCAAGAACCCCAAGATAATGCCACAGGGACAAAGAGGGAT 420
QY 421 GACCAGAGTCATTGGCGCTATGGAGGCGACCCCGCCCTGGCCCGGCTGCTCCAGCCTGC 480
Db GACCAGAGTCATTGGCGCTATGGAGGCGACCCCGCCCTGGCCCGGCTGCTCCAGCCTGC 480
QY 481 GCGGGCCGCTTCCAGTCCCGGTGGATATCCGCCCCCAGCTCGCCCGCTTCTGCCCCGCC 540
Db GCGGGCCGCTTCCAGTCCCGGTGGATATCCGCCCCCAGCTCGCCCGCTTCTGCCCCGCC 540
QY 541 CTGCGCCCCCTGGAACTCTCTGGGCTTCCAGCTCCCGCCGCTCCAGAACTGGCCCTGCGC 600
Db CTGCGCCCCCTGGAACTCTCTGGGCTTCCAGCTCCCGCCGCTCCAGAACTGGCCCTGCGC 600
QY 601 AACAAATGGCCACAGTGTGCAACTGACCTGCTCTGGGGCTAGAGATGGTCTGGGTCCC 660
Db AACAAATGGCCACAGTGTGCAACTGACCTGCTCTGGGGCTAGAGATGGTCTGGGTCCC 660
QY 661 GGGGGGAGTACCGGGCTGTGCACTGCACTGGGGGCTGCAAGTGGTCTGGGTCCC 720
Db GGGGGGAGTACCGGGCTGTGCACTGCACTGGGGGCTGCAAGTGGTCTGGGTCCC 720
QY 721 TCGGAGCACACTGTGGAGGCCACCGTTTCCCTGCGGAGATCCACGTGGTTTACCTCAGC 780
Db TCGGAGCACACTGTGGAGGCCACCGTTTCCCTGCGGAGATCCACGTGGTTTACCTCAGC 780

CC prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell
CC cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous
CC cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's
CC tumour
XX
SQ Sequence 1552 BP; 302 A; 471 C; 461 G; 318 T; 0 U; 0 Other;

Query Match 100.0%; Score 1522; DB 6; Length 1552;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACAGTCAGCCGCATGGCTCCCTGTGCCCCAGCCCTGGCTCCCTCTGTGTGATCCCGGCC 60
Db 31 ACAGTCAGCCGCATGGCTCCCTGTGCCCCAGCCCTGGCTCCCTCTGTGTGATCCCGGCC 90
QY 61 CTTGCTCCAGGCCCTCACTGTGCAACTGCTGCTGTCACTGCTGCTTCTGATGCCCTGTCCAT 120
Db 91 CTTGCTCCAGGCCCTCACTGTGCAACTGCTGCTGTCACTGCTGCTTCTGATGCCCTGTCCAT 150
QY 121 CCCAGAGGTTGCCCGGATGTCAGGAGGATTTCCCCCTTGGGAGGAGGCTCTTCTGGGGAA 180
Db 151 CCCAGAGGTTGCCCGGATGTCAGGAGGATTTCCCCCTTGGGAGGAGGCTCTTCTGGGGAA 210
QY 181 GATGACCCACTGGCGGAGGAGGATCTACCTGGAGAGGAGGATTCACCCAGAGAGGAGAT 240
Db 211 GATGACCCACTGGCGGAGGAGGATCTACCTGGAGAGGAGGATTCACCCAGAGAGGAGAT 270
QY 241 CCACCCGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCT 300
Db 271 CCACCCGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCT 330
QY 301 GAAGTTAAGCCCTAAATCAGAAGAAAGAGGGCTCCCTGAAAGTTAGAGGATCTACCTACTGTT 360
Db 331 GAAGTTAAGCCCTAAATCAGAAGAAAGAGGGCTCCCTGAAAGTTAGAGGATCTACCTACTGTT 390
QY 361 GAGGCTCCTGGAGATCCTCAAGAACCCAGAAATATGCCCCACAGGGACAAAGAGGGGAT 420
Db 391 GAGGCTCCTGGAGATCCTCAAGAACCCAGAAATATGCCCCACAGGGACAAAGAGGGGAT 450
QY 421 GACCAGAGTCATTGGCGCTATGGAGGCGACCCGCCCTGGCCCCCGGGTGTCCCCAGCCTGC 480
Db 451 GACCAGAGTCATTGGCGCTATGGAGGCGACCCGCCCTGGCCCCCGGGTGTCCCCAGCCTGC 510
QY 481 GCGGCGCGCTTCCAGTCCCGGTGGATATCCGCCCCAGCTCGCCGCTTCTGCCCGGCC 540
Db 511 GCGGCGCGCTTCCAGTCCCGGTGGATATCCGCCCCAGCTCGCCGCTTCTGCCCGGCC 570
QY 541 CTGCGCCCCCTGGAACCTCTGGGCTTCCAGCTCCCGCCGCTCCAGAACTGCGCTGCGC 600
Db 571 CTGCGCCCCCTGGAACCTCTGGGCTTCCAGCTCCCGCCGCTCCAGAACTGCGCTGCGC 630
QY 601 AACATGGCCACAGTGTGCAACTGACCCCTGCTTCCAGCTCCCGCCGCTCCAGAACTGCGTCCC 660
Db 631 AACATGGCCACAGTGTGCAACTGACCCCTGCTTCCAGCTCCCGCCGCTCCAGAACTGCGTCCC 690
QY 661 GGGCGGGAGTACCGGGCTCTGCAGCTGCATCTGCACTGGGGGGCTGCAGGTGCTCCGGGC 720
Db 691 GGGCGGGAGTACCGGGCTCTGCAGCTGCATCTGCACTGGGGGGCTGCAGGTGCTCCGGGC 750
QY 721 TCGAGACACACTGTGGAAGGCCACCGTTTCCCTGCGAGATCCACGTGTTTCACTCAGC 780
Db 751 TCGAGACACACTGTGGAAGGCCACCGTTTCCCTGCGAGATCCACGTGTTTCACTCAGC 810
QY 781 ACCGCTTTGCCAGAGTTGACGAGGCCCTTGGGGCGCCCGGAGGCCCTGGCGGTGTTGGCC 840
Db 811 ACCGCTTTGCCAGAGTTGACGAGGCCCTTGGGGCGCCCGGAGGCCCTGGCGGTGTTGGCC 870
QY 841 GCCTTTCTGAGGAGGGGCCCGGAAGAAACAGTGCCTATGAGCAGTTGCTGCTCGCTTG 900
Db 871 GCCTTTCTGAGGAGGGGCCCGGAAGAAACAGTGCCTATGAGCAGTTGCTGCTCGCTTG 930
QY 901 GAAGAAATCGTGAGGAAGGCTCAGAGACTCAGGTCCCAGGACTGGACATATCTGCACTC 960

Db 931 GAAGAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCAGGACTGGACATATCTGCACTC 990
QY 961 CTGCCCTCTGACTTCAGCCCGCTACTTCCAATATGAGGGGTCTCTGACTACACCGCCCTGT 1020
Db 991 CTGCCCTCTGACTTCAGCCCGCTACTTCCAATATGAGGGGTCTCTGACTACACCGCCCTGT 1050
QY 1021 GCCCAGGGTGTCTATCTGGACTGTGTTTAAACCAGACAGTGTCTGAGTGTCTAAGCAGCTC 1080
Db 1051 GCCCAGGGTGTCTATCTGGACTGTGTTTAAACCAGACAGTGTCTGAGTGTCTAAGCAGCTC 1110
QY 1081 CACACCCCTCTCTGACACACCCTGTGGGACCTTGGTGAATCTCGGCTACAGTGAATTCCTCGA 1140
Db 1111 CACACCCCTCTCTGACACACCCTGTGGGACCTTGGTGAATCTCGGCTACAGTGAATTCCTCGA 1170
QY 1141 GCGACGCAGCCTTTGAATGGCGAGTGAATGAGGCCCTCCTTCCCTGCTGAGTGGACAGC 1200
Db 1171 GCGACGCAGCCTTTGAATGGCGAGTGAATGAGGCCCTCCTTCCCTGCTGAGTGGACAGC 1230
QY 1201 AGTCCTCGGGCTGCTGAGCCAGTCCAGCTGAATTCCTGCTGGTGGTGTGACATCCTA 1260
Db 1231 AGTCCTCGGGCTGCTGAGCCAGTCCAGCTGAATTCCTGCTGGTGGTGTGACATCCTA 1290
QY 1261 GCGCTGGTTTTTGGCCTCCTTTTGTGTGTCAACAGCGTCCGCTTCCCTTGTGCAGATGAGA 1320
Db 1291 GCGCTGGTTTTTGGCCTCCTTTTGTGTGTCAACAGCGTCCGCTTCCCTTGTGCAGATGAGA 1350
QY 1321 AGGCAGCACAGAAGGGGAACCAAGGGGGTGTGAGCTACCGCCCAGCAGAGGTAGCCGAG 1380
Db 1351 AGGCAGCACAGAAGGGGAACCAAGGGGGTGTGAGCTACCGCCCAGCAGAGGTAGCCGAG 1410
QY 1381 ACTGGAGCCTAGAGCTGGATCTTGGAGATGTGAGAAAGCCAGCCAGGSCATCTGAGGG 1440
Db 1411 ACTGGAGCCTAGAGCTGGATCTTGGAGATGTGAGAAAGCCAGCCAGGSCATCTGAGGG 1470
QY 1441 GGAGCCGGTAACTGCTGCTGCTGCTCATTATGCCCACCTTCTTTTAACTGCCAAGAAATT 1500
Db 1471 GGAGCCGGTAACTGCTGCTGCTGCTCATTATGCCACCTTCTTTTAACTGCCAAGAAATT 1530
QY 1501 TTTTAAATAAATAATTTATAAT 1522
Db 1531 TTTTAAATAAATAATTTATAAT 1552

RESULT 5

ABL62179
ID ABL62179 standard; DNA; 1552 BP.

XX ABL62179;

XX 15-MAY-2002 (first entry)

XX Colon adenocarcinoma related gene sequence SEQ ID NO:516.

DE Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
KW gene; ds.

OS Homo sapiens.

XX WO200194629-A2.

XX 13-DEC-2001.

XX 30-MAY-2001; 2001WO-US010838.

XX 05-JUN-2000; 2000US-0209473P.

PR 05-JUN-2000; 2000US-0209531P.

PR 18-SEP-2000; 2000US-0233133P.

PR 18-SEP-2000; 2000US-0233617P.

PR 20-SEP-2000; 2000US-0234009P.

PR 20-SEP-2000; 2000US-0234034P.

PR 20-SEP-2000; 2000US-0234052P.

PR 22-SEP-2000; 2000US-0234509P.
PR 22-SEP-2000; 2000US-0234567P.
PR 25-SEP-2000; 2000US-0234923P.
PR 25-SEP-2000; 2000US-0234924P.
PR 25-SEP-2000; 2000US-0235077P.
PR 25-SEP-2000; 2000US-0235082P.
PR 25-SEP-2000; 2000US-0235134P.
PR 25-SEP-2000; 2000US-0235280P.
PR 26-SEP-2000; 2000US-0235637P.
PR 26-SEP-2000; 2000US-0235638P.
PR 27-SEP-2000; 2000US-0235711P.
PR 27-SEP-2000; 2000US-0235720P.
PR 27-SEP-2000; 2000US-0235840P.
PR 27-SEP-2000; 2000US-0235863P.
PR 28-SEP-2000; 2000US-0236028P.
PR 28-SEP-2000; 2000US-0236032P.
PR 28-SEP-2000; 2000US-0236033P.
PR 28-SEP-2000; 2000US-0236034P.
PR 28-SEP-2000; 2000US-0236109P.
PR 28-SEP-2000; 2000US-0236111P.
PR 29-SEP-2000; 2000US-0236842P.
PR 29-SEP-2000; 2000US-0236891P.
PR 02-OCT-2000; 2000US-0237172P.
PR 02-OCT-2000; 2000US-0237173P.
PR 02-OCT-2000; 2000US-0237278P.
PR 02-OCT-2000; 2000US-0237294P.
PR 02-OCT-2000; 2000US-0237295P.
PR 02-OCT-2000; 2000US-0237316P.
PR 03-OCT-2000; 2000US-0237425P.
PR 03-OCT-2000; 2000US-0237598P.
PR 03-OCT-2000; 2000US-0237604P.
PR 03-OCT-2000; 2000US-0237606P.
PR 03-OCT-2000; 2000US-0237608P.
PR 01-NOV-2000; 2000US-0244867P.
PR 01-NOV-2000; 2000US-0245084P.

(AVAL-) AVALON PHARM.

Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
Soppet DR, Weaver Z;
WPI; 2002-188264/24.

Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set.

Claim 1; SEQ ID NO 516; 44pp; English.

The present invention describes a method (M1) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in ABL51664 to ABL70110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. M1 can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of M1, and the data is sufficient to convey the chemical structure and/or properties of the agent. M1 can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's tumour

Sequence 1552 BP; 302 A; 471 C; 461 G; 318 T; 0 U; 0 Other;

Query Match 100.0%; Score 1522; DB 6; Length 1552;
Best Local Similarity 100.0%; Pred. NO. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACAGTCAGCCGCGATGGCTCCCTGTGCCCCAGCCCTGGCTCCCTCTGTGATCCCGGCC 60
Db |||||
31 ACAGTCAGCCGCGATGGCTCCCTGTGCCCCAGCCCTGGCTCCCTCTGTGATCCCGGCC 90
QY 61 CCTGCTCCAGGCTCACTGTGCAACTGCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 120
Db |||||
91 CCTGCTCCAGGCTCACTGTGCAACTGCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 150
QY 121 CCCAGAGGTTGCCCGGATGCAGGAGGATTCCTTGGGAGGAGGCTCTTCTGGGGAA 180
Db |||||
151 CCCAGAGGTTGCCCGGATGCAGGAGGATTCCTTGGGAGGAGGCTCTTCTGGGGAA 210
QY 181 GATGACCCACTGGGCGAGGAGGATCTGCCAGTGAAGAGGATTCACCCAGAGAGGAGAT 240
Db |||||
211 GATGACCCACTGGGCGAGGAGGATCTGCCAGTGAAGAGGATTCACCCAGAGAGGAGAT 270
QY 241 CCACCCGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCT 300
Db |||||
271 CCACCCGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCT 330
QY 301 GAAGTTAAGCCTAAATCAGAAGAGAGGGCTCCCTGAAAGTTAGAGGATCTACCTACTGTT 360
Db |||||
331 GAAGTTAAGCCTAAATCAGAAGAGAGGGCTCCCTGAAAGTTAGAGGATCTACCTACTGTT 390
QY 361 GAGGCTCCTGGAGATCCTCAAGAACCCAGAAATAATGCCACAGGACAAAAGAGGGAT 420
Db |||||
391 GAGGCTCCTGGAGATCCTCAAGAACCCAGAAATAATGCCACAGGACAAAAGAGGGAT 450
QY 421 GACCAGAGTCATTGGCGCTATGGAGGCGACCCCGCTGGCCCCGGTGTCCCCAGCCTGC 480
Db |||||
451 GACCAGAGTCATTGGCGCTATGGAGGCGACCCCGCTGGCCCCGGTGTCCCCAGCCTGC 510
QY 481 GCGGGCGCTTCCAGTCCCGGTGGATATCCGCCGCCAGCTCGCGCCCTTCTGCCCGGCC 540
Db |||||
511 GCGGGCGCTTCCAGTCCCGGTGGATATCCGCCGCCAGCTCGCGCCCTTCTGCCCGGCC 570
QY 541 CTGCGCCCCCTGGAACTCTTGGGCTTCAGACTCCGCCGCTCCAGAACTGCGCCTGCGC 600
Db |||||
571 CTGCGCCCCCTGGAACTCTTGGGCTTCAGACTCCGCCGCTCCAGAACTGCGCCTGCGC 630
QY 601 AACAAATGGCCACAGTGTGCAACTGACCTGCTCCCTGCGGCTAGAGATGGCTCTGGGTCCC 660
Db |||||
631 AACAAATGGCCACAGTGTGCAACTGACCTGCTCCCTGCGGCTAGAGATGGCTCTGGGTCCC 690
QY 661 GGGCGGGAGTACCGGGCTCTGCAGCTGCATCTGCAGTGGGGGCTGCAGGTGTCGCGGCC 720
Db |||||
691 GGGCGGGAGTACCGGGCTCTGCAGCTGCATCTGCAGTGGGGGCTGCAGGTGTCGCGGCC 750
QY 721 TCGGAGCACACTGTGGAAGGCCACCGTTTCCCTGCCGAGATCCACCTGGTTTCACTCAGC 780
Db |||||
751 TCGGAGCACACTGTGGAAGGCCACCGTTTCCCTGCCGAGATCCACCTGGTTTCACTCAGC 810
QY 781 ACCGCTTTTGCAGAGTTGACGAGGCTTGGGGCGCCCGGGAGGCTGGCCCGTGTGGCC 840
Db |||||
811 ACCGCTTTTGCAGAGTTGACGAGGCTTGGGGCGCCCGGGAGGCTGGCCCGTGTGGCC 870
QY 841 GCCTTTTCTGGAGGGGCCCGGAAGAAACAGTGCCTATGAGCAGTTGCTGTCTCGCTTG 900
Db |||||
871 GCCTTTTCTGGAGGGGCCCGGAAGAAACAGTGCCTATGAGCAGTTGCTGTCTCGCTTG 930
QY 901 GAAGAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCCAGGACTGGACATATCTGCACCTC 960
Db |||||
931 GAAGAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCCAGGACTGGACATATCTGCACCTC 990
QY 961 CTGCCCTCTGACTTCAGCCGCTACTTCCATATGAGGGGTCTCTGACTACACCCGCTGT 1020
Db |||||
991 CTGCCCTCTGACTTCAGCCGCTACTTCCATATGAGGGGTCTCTGACTACACCCGCTGT 1050
QY 1021 GCCCAGGGTGTCTGACTGTGGTGTATTAACCAGACAGTGTGCTGACTGCTAAGCAGCTC 1080
Db |||||
1051 GCCCAGGGTGTCTGACTGTGGTGTATTAACCAGACAGTGTGCTGACTGCTAAGCAGCTC 1110
QY 1081 CACACCTCTCTGACACACCTGTGGGGACCTGGGTGACTCTCGGCTACAGCTGAACTTCCGA 1140

Db 1111 CACACCCCTCTGTGACACCCCTGTGGGACCTGGTGACTCTGGCTACAGCTGAACCTCCGA 1170
Qy 1141 GCGACGAGCCTTTGAATGGCGAGTGAATTGAGGCCTCTCCCTGCTGGAGTGACAGC 1200
Db 1171 GCGACGAGCCTTTGAATGGCGAGTGAATTGAGGCCTCTCCCTGCTGGAGTGACAGC 1230
Qy 1201 AGTCCTGGGCTGCTGAGCCAGTCCAGCTGAATTCCTGCTGGCTGCTGGTGACATCCTA 1260
Db 1231 AGTCCTGGGCTGCTGAGCCAGTCCAGCTGAATTCCTGCTGGCTGCTGGTGACATCCTA 1290
Qy 1261 GCCCTGGTTTGGCCTCCTTTTGTGCTGTCAACGCGTCCGCTTCCCTTGTGCAGATGAGA 1320
Db 1291 GCCCTGGTTTGGCCTCCTTTTGTGCTGTCAACGCGTCCGCTTCCCTTGTGCAGATGAGA 1350
Qy 1321 AGGCAGCACAGAAGGGGAACCAAGGGGTGTGAGCTACCGCCAGCAGAGGTAGCCGAG 1380
Db 1351 AGGCAGCACAGAAGGGGAACCAAGGGGTGTGAGCTACCGCCAGCAGAGGTAGCCGAG 1410
Qy 1381 ACTGGAGCCTAGAGGCTGGATCTTGGAGAAATGTGAGAAGCCAGCCAGAGGCATCTGAGGG 1440
Db 1411 ACTGGAGCCTAGAGGCTGGATCTTGGAGAAATGTGAGAAGCCAGCCAGAGGCATCTGAGGG 1470
Qy 1441 GGAGCCGGTAACTGCTCTGCTGCTCATTTATGCCACTTCTTTTAACTGCCAAGAAATT 1500
Db 1471 GGAGCCGGTAACTGCTCTGCTGCTCATTTATGCCACTTCTTTTAACTGCCAAGAAATT 1530
Qy 1501 TTTTAAATAAATAATTATTAAT 1522
Db 1531 TTTTAAATAAATAATTATTAAT 1552

RESULT 6
ABL65416
ID ABL65416 standard; DNA; 1552 BP.
XX ABL65416;
XX
DT 15-MAY-2002 (first entry)
XX
DE Lung cancer related gene sequence SEQ ID NO:3753.
XX
KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
KW gene; ds.
XX
OS Homo sapiens.
XX
PN WO200194629-A2.
XX
PD 13-DEC-2001.
XX
PF 30-MAY-2001; 2001WO-US010838.
XX

PR 05-JUN-2000; 2000US-0209473P.
PR 05-JUN-2000; 2000US-0209531P.
PR 18-SEP-2000; 2000US-0233133P.
PR 18-SEP-2000; 2000US-0233617P.
PR 20-SEP-2000; 2000US-0234009P.
PR 20-SEP-2000; 2000US-0234034P.
PR 20-SEP-2000; 2000US-0234052P.
PR 22-SEP-2000; 2000US-0234509P.
PR 22-SEP-2000; 2000US-0234567P.
PR 25-SEP-2000; 2000US-0234923P.
PR 25-SEP-2000; 2000US-0234924P.
PR 25-SEP-2000; 2000US-0235077P.
PR 25-SEP-2000; 2000US-0235082P.
PR 25-SEP-2000; 2000US-0235134P.
PR 25-SEP-2000; 2000US-0235280P.
PR 26-SEP-2000; 2000US-0235637P.
PR 26-SEP-2000; 2000US-0235638P.
PR 27-SEP-2000; 2000US-0235711P.

PR 27-SEP-2000; 2000US-0235720P.
PR 27-SEP-2000; 2000US-0235840P.
PR 27-SEP-2000; 2000US-0235863P.
PR 28-SEP-2000; 2000US-0236028P.
PR 28-SEP-2000; 2000US-0236032P.
PR 28-SEP-2000; 2000US-0236033P.
PR 28-SEP-2000; 2000US-0236034P.
PR 28-SEP-2000; 2000US-0236109P.
PR 28-SEP-2000; 2000US-0236111P.
PR 29-SEP-2000; 2000US-0236842P.
PR 29-SEP-2000; 2000US-0236891P.
PR 02-OCT-2000; 2000US-0237172P.
PR 02-OCT-2000; 2000US-0237173P.
PR 02-OCT-2000; 2000US-0237278P.
PR 02-OCT-2000; 2000US-0237294P.
PR 02-OCT-2000; 2000US-0237295P.
PR 02-OCT-2000; 2000US-0237316P.
PR 03-OCT-2000; 2000US-0237425P.
PR 03-OCT-2000; 2000US-0237598P.
PR 03-OCT-2000; 2000US-0237604P.
PR 03-OCT-2000; 2000US-0237606P.
PR 03-OCT-2000; 2000US-0237608P.
PR 01-NOV-2000; 2000US-0244867P.
PR 01-NOV-2000; 2000US-0245084P.
XX
PA (AVAL-) AVALON PHARM.
XX
PI Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
PI Soppet DR, Weaver Z;
XX
DR WPI; 2002-188264/24.
XX
PT Screening for anti-neoplastic agent involves exposing cells to a chemical
PT agent to be tested for anti-neoplastic activity, and determining a change
PT in expression of a gene of a signature gene set.
XX
PS Claim 1; SEQ ID NO 3753; 44pp; English.
XX
CC The present invention describes a method (M1) for screening for an anti-
CC neoplastic agent. The method involves exposing cells to a chemical agent
CC to be tested for anti-neoplastic activity, determining a change in
CC expression of at least one gene (I) of a signature gene set, where (I)
CC comprises a sequence (S) selected from 847 sequences (given in ABL61664
CC to ABL70110), or is at least 95% identical to (S), where a change in
CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC activity and can be used in gene therapy. M1 can be used for screening an
CC anti-neoplastic agent, and can be used for producing a product which is
CC the data collected with respect to the anti-neoplastic agent as a result
CC of M1, and the data is sufficient to convey the chemical structure and/or
CC properties of the agent. M1 can be used in the treatment of cancer such
CC as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,
CC prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell
CC cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous
CC cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's
CC tumour
XX
SQ Sequence 1552 BP; 302 A; 471 C; 461 G; 318 T; 0 U; 0 Other;
Query Match 100.0%; Score 1522; DB 6; Length 1552;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ACAGTCAGCCGATGGCTCCCTGTGCCCCAGCCCTGGCTCCCTCTGTGTGATCCCGCC 60
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
31 ACAGTCAGCCGATGGCTCCCTGTGCCCCAGCCCTGGCTCCCTCTGTGTGATCCCGCC 90
Qy 61 CCTGCTCCAGGCCCTCACTGTGCAACTGTCTGTCACTGTCTTCTGATGCTGTCCAT 120
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
91 CCTGCTCCAGGCCCTCACTGTGCAACTGTCTGTCACTGTCTTCTGATGCTGTCCAT 150
Qy 121 CCCAGAGGTTGCCCGGATGCAGGAGGATTCCCCCTTGGGAGGAGGCTCTTCTGGGAA 180
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
151 CCCAGAGGTTGCCCGGATGCAGGAGGATTCCCCCTTGGGAGGAGGCTCTTCTGGGAA 210

QY 181 GATGACCCACTGGGCGAGGAGGATCTGCCCAGTGAAGAGGATTCACCCAGAGAGGAGGAT 240
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
211 GATGACCCACTGGGCGAGGAGGATCTGCCCAGTGAAGAGGATTCACCCAGAGAGGAGGAT 270
QY 241 CCACCCGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACTGGAGAGGAGGATCTACCT 300
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
271 CCACCCGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACTGGAGAGGAGGATCTACCT 330
QY 301 GAAAGTTAAGCCTAAANTCAGAAGAACAGAGGGCTCCCTGAAGTTAGAGGATCTACCTACTGTT 360
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
331 GAAAGTTAAGCCTAAANTCAGAAGAACAGAGGGCTCCCTGAAGTTAGAGGATCTACCTACTGTT 390
QY 361 GAGGCTCCTGGAGATCCTCAAGAACCCAGAAATAATGCCACAGGGACAAAGAGGGGAT 420
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
391 GAGGCTCCTGGAGATCCTCAAGAACCCAGAAATAATGCCACAGGGACAAAGAGGGGAT 450
QY 421 GACCAGAGTCATTGGCGCTATGGAGGGACCCCGCCCTGGCCCCGGGTGTCCCCAGCCTGC 480
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
451 GACCAGAGTCATTGGCGCTATGGAGGGACCCCGCCCTGGCCCCGGGTGTCCCCAGCCTGC 510
QY 481 GCGGGCCGCTTCAGTCCCGGTGGATATCCGCCCCCGCCAGCTCGCCGCCCTTCTGCCCCGCC 540
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
511 GCGGGCCGCTTCAGTCCCGGTGGATATCCGCCCCCGCCAGCTCGCCGCCCTTCTGCCCCGCC 570
QY 541 CTGCGCCCCCTGGAACTCCTGGGCTTCAGCTCCCGCCGCTCCAGAACTGCGCCTGCGC 600
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
571 CTGCGCCCCCTGGAACTCCTGGGCTTCAGCTCCCGCCGCTCCAGAACTGCGCCTGCGC 630
QY 601 AACAAATGGCCACAGTGTGCAACTGACCTCGCTCCTGGGCTAGAGATGGCTCTGGGTCCC 660
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
631 AACAAATGGCCACAGTGTGCAACTGACCTCGCTCCTGGGCTAGAGATGGCTCTGGGTCCC 690
QY 661 GGGCGGGAGTACCGGGCTCTGCAGCTGCACTGCGGGGGCTGCAGGTGCTCGCGGGC 720
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
691 GGGCGGGAGTACCGGGCTCTGCAGCTGCACTGCGGGGGCTGCAGGTGCTCGCGGGC 750
QY 721 TCGGAGCACACTGTGGAAGGCCACCGTTTCCCTGCCGAGATCCACGTGGTTCACTCAGC 780
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
751 TCGGAGCACACTGTGGAAGGCCACCGTTTCCCTGCCGAGATCCACGTGGTTCACTCAGC 810
QY 781 ACCGCCCTTGCCAGAGTTGACGAGGCCCTGGGGCGCCCGGAGGCCCTGGCCGTTGGCC 840
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
811 ACCGCCCTTGCCAGAGTTGACGAGGCCCTGGGGCGCCCGGAGGCCCTGGCCGTTGGCC 870
QY 841 GCCTTTCTGGAGAGGGCCCGGAAGAAACAGTGCCTATGACAGTTGCTGTCTCGCTG 900
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
871 GCCTTTCTGGAGAGGGCCCGGAAGAAACAGTGCCTATGACAGTTGCTGTCTCGCTG 930
QY 901 GAAGAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCCAGGACTGGACATATCTGCACTC 960
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
931 GAAGAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCCAGGACTGGACATATCTGCACTC 990
QY 961 CTGCCCTCTGACTTCAGCCGCTACTTCCAATATGAGGGGTCTCTGACTACACCCGCCCTGT 1020
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
991 CTGCCCTCTGACTTCAGCCGCTACTTCCAATATGAGGGGTCTCTGACTACACCCGCCCTGT 1050
QY 1021 GCCCAGGGTGCATCTGGACTGTGTTTAAACCAGACAGTGTGCTGAGTGTAAAGCAGCTC 1080
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1051 GCCCAGGGTGCATCTGGACTGTGTTTAAACCAGACAGTGTGCTGAGTGTAAAGCAGCTC 1110
QY 1081 CACACCCCTCTTGACACCCCTGTGGGAGCTGGTGACTCTCGGTACAGCTGAACCTTCCGA 1140
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1111 CACACCCCTCTTGACACCCCTGTGGGAGCTGGTGACTCTCGGTACAGCTGAACCTTCCGA 1170
QY 1141 GCGACGCAGCCTTTGAATGGGCGAGTGAATGAGGCCTCCTTCCCTGCTGGAGTGGACAGC 1200
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1171 GCGACGCAGCCTTTGAATGGGCGAGTGAATGAGGCCTCCTTCCCTGCTGGAGTGGACAGC 1230
QY 1201 AGTCCTCGGGCTGCTGAGCCAGTCCAGCTGAATTCCTGCCCTGGCTGCTGGTGACATCCTA 1260
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1231 AGTCCTCGGGCTGCTGAGCCAGTCCAGCTGAATTCCTGCCCTGGCTGCTGGTGACATCCTA 1290

QY 1261 GCCCTGGTTTTTGGCCTCCTTTTGTGCTGTCAACGAGCGTCGGGTTCTTGTGCAGATGAGA 1320
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1291 GCCCTGGTTTTTGGCCTCCTTTTGTGCTGTCAACGAGCGTCGGGTTCTTGTGCAGATGAGA 1350
QY 1321 AGGCAGCACAGAAGGGGAACCAAGGGGGTGTGAGCTACCGCCAGAGGAGGTAGCCGAG 1380
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1351 AGGCAGCACAGAAGGGGAACCAAGGGGGTGTGAGCTACCGCCAGAGGAGGTAGCCGAG 1410
QY 1381 ACTGGAGCCTAGAGGCTGGATCTTTGGAGAATGTGAGAAGCCAGAGGCGCATCTGAGGG 1440
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1411 ACTGGAGCCTAGAGGCTGGATCTTTGGAGAATGTGAGAAGCCAGAGGCGCATCTGAGGG 1470
QY 1441 GGAGCCGGTAACTGTCTGTCTGCTCATTATGCCACTTCTCTTTAACTGCCAAGAAATT 1500
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1471 GGAGCCGGTAACTGTCTGTCTGCTCATTATGCCACTTCTCTTTAACTGCCAAGAAATT 1530
QY 1501 TTTTAAATAAATAATTTTATAAT 1522
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1531 TTTTAAATAAATAATTTTATAAT 1552

RESULT 7
ABL68346
ID ABL68346 standard; DNA; 1552 BP.
XX
AC ABL68346;
XX
DT 15-MAY-2002 (first entry)
XX
DE Kidney cancer related gene sequence SEQ ID NO:6683.
XX
KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
KW gene; ds.
OS Homo sapiens.
XX
PN WO200194629-A2.
XX
PD 13-DEC-2001.
XX
PF 30-MAY-2001; 2001WO-US010838.
XX
PR 05-JUN-2000; 2000US-0209473P.
PR 05-JUN-2000; 2000US-0209531P.
PR 18-SEP-2000; 2000US-0233133P.
PR 18-SEP-2000; 2000US-0233617P.
PR 20-SEP-2000; 2000US-0234009P.
PR 20-SEP-2000; 2000US-0234034P.
PR 20-SEP-2000; 2000US-0234052P.
PR 22-SEP-2000; 2000US-0234509P.
PR 22-SEP-2000; 2000US-0234567P.
PR 25-SEP-2000; 2000US-0234923P.
PR 25-SEP-2000; 2000US-0234924P.
PR 25-SEP-2000; 2000US-0235077P.
PR 25-SEP-2000; 2000US-0235082P.
PR 25-SEP-2000; 2000US-0235134P.
PR 25-SEP-2000; 2000US-0235280P.
PR 26-SEP-2000; 2000US-0235637P.
PR 26-SEP-2000; 2000US-0235638P.
PR 27-SEP-2000; 2000US-0235711P.
PR 27-SEP-2000; 2000US-0235720P.
PR 27-SEP-2000; 2000US-0235840P.
PR 27-SEP-2000; 2000US-0235863P.
PR 28-SEP-2000; 2000US-0236028P.
PR 28-SEP-2000; 2000US-0236032P.
PR 28-SEP-2000; 2000US-0236033P.
PR 28-SEP-2000; 2000US-0236034P.
PR 28-SEP-2000; 2000US-0236109P.
PR 28-SEP-2000; 2000US-0236111P.
PR 29-SEP-2000; 2000US-0236842P.
PR 29-SEP-2000; 2000US-0236891P.

PR 02-OCT-2000; 2000US-0237172P.
PR 02-OCT-2000; 2000US-0237173P.
PR 02-OCT-2000; 2000US-0237278P.
PR 02-OCT-2000; 2000US-0237294P.
PR 02-OCT-2000; 2000US-0237295P.
PR 02-OCT-2000; 2000US-0237316P.
PR 03-OCT-2000; 2000US-0237425P.
PR 03-OCT-2000; 2000US-0237598P.
PR 03-OCT-2000; 2000US-0237604P.
PR 03-OCT-2000; 2000US-0237606P.
PR 03-OCT-2000; 2000US-0237608P.
PR 01-NOV-2000; 2000US-0244867P.
PR 01-NOV-2000; 2000US-0245084P.
XX
PA (AVAL-) AVALON PHARM.
XX
PI Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
PI Soppet DR, Weaver Z;
XX
DR WPI; 2002-188264/24.
XX
PT Screening for anti-neoplastic agent involves exposing cells to a chemical
PT agent to be tested for anti-neoplastic activity, and determining a change
PT in expression of a gene of a signature gene set.
XX
PS Claim 1; SEQ ID NO 6683; 44pp; English.
XX
CC The present invention describes a method (M1) for screening for an anti-
CC neoplastic agent. The method involves exposing cells to a chemical agent
CC to be tested for anti-neoplastic activity, determining a change in
CC expression of at least one gene (I) of a signature gene set, where (I)
CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664
CC to ABL70110), or is at least 95% identical to (S), where a change in
CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC activity and can be used in gene therapy. M1 can be used for screening an
CC anti-neoplastic agent, and can be used for producing a product which is
CC the data collected with respect to the anti-neoplastic agent as a result
CC of M1, and the data is sufficient to convey the chemical structure and/or
CC properties of the agent. M1 can be used in the treatment of cancer such
CC as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,
CC prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell
CC cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous
CC cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's
CC tumour
XX
SQ Sequence 1552 BP; 302 A; 471 C; 461 G; 318 T; 0 U; 0 Other;
Query Match 100.0%; Score 1522; DB 6; Length 1552;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACAGTCAGCCGCGATGGCTCCCTGTGCCCCAGCCCTGGCTCCCTCTGTGATCCCGGCC 60
Db |||||
QY 31 ACAGTCAGCCGCGATGGCTCCCTGTGCCCCAGCCCTGGCTCCCTCTGTGATCCCGGCC 90
Db |||||
QY 61 CCTGCTCCAGGCCCTCACTGTGCAACTGCTGCTGTCACTGCTGCTTCTGATGCTGCCAT 120
Db |||||
QY 91 CCTGCTCCAGGCCCTCACTGTGCAACTGCTGCTGTCACTGCTGCTTCTGATGCTGCCAT 150
Db |||||
QY 121 CCCAGAGGTTGCCCGGAGGAGGATCTGCCAGTGAAGAGGATTCACCCAGAGAGGAGAT 180
Db |||||
QY 151 CCCAGAGGTTGCCCGGAGGAGGATTCGCCAGTGAAGAGGATTCACCCAGAGAGGAGAT 210
Db |||||
QY 181 GATGACCACTGGGCGAGGAGGATCTGCCAGTGAAGAGGATTCACCCAGAGAGGAGAT 240
Db |||||
QY 211 GATGACCACTGGGCGAGGAGGATCTGCCAGTGAAGAGGATTCACCCAGAGAGGAGAT 270
Db |||||
QY 241 CCACCCGAGAGGAGGATCTACCTGGAGAGGAGATCTACCTGGAGAGGAGGATCTACCT 300
Db |||||
QY 271 CCACCCGAGAGGAGGATCTACCTGGAGAGGAGATCTACCTGGAGAGGAGGATCTACCT 330
Db |||||
QY 301 GAAGTTAAGCCTAAATCAGAAGAGAGGGCTCCCTGAAGTTAGAGGATCTACCTACTGTT 360
Db |||||

Db 331 GAAGTTAAGCCTAAATCAGAAGAGAGGGCTCCCTGAAGTTAGAGGATCTACCTACTGTT 390
QY 361 GAGGCTCCTGGAGATCCTCAAGAACCCCAAGATAAATGCCACAGGGAAGAGGGAT 420
Db |||||
QY 391 GAGGCTCCTGGAGATCCTCAAGAACCCCAAGATAAATGCCACAGGGAAGAGGGAT 450
Db |||||
QY 421 GACCAGAGTCAATTGGCGCTATGGAGGCGACCCCGCTGGCCCGGGTGTCTCCAGCCTGC 480
Db |||||
QY 451 GACCAGAGTCAATTGGCGCTATGGAGGCGACCCCGCTGGCCCGGGTGTCTCCAGCCTGC 510
Db |||||
QY 481 GCGGGCCGCTTCCAGTCCCGGTGGATATCGCCCCCAGCTCGCCCGCTTCTGCCCGGCC 540
Db |||||
QY 511 GCGGGCCGCTTCCAGTCCCGGTGGATATCGCCCCCAGCTCGCCCGCTTCTGCCCGGCC 570
Db |||||
QY 541 CTGCGCCCCCTGGAACTCCTGGGCTTCCAGTCCCGCCGCTCCCAAGAACTGCGCCTGCGC 600
Db |||||
QY 571 CTGCGCCCCCTGGAACTCCTGGGCTTCCAGTCCCGCCGCTCCCAAGAACTGCGCCTGCGC 630
Db |||||
QY 601 AACAAATGGCCACAGTGTGCAACTGACCTGCTCCCTGGGCTAGAGATGGCTCTGGGTCCC 660
Db |||||
QY 631 AACAAATGGCCACAGTGTGCAACTGACCTGCTCCCTGGGCTAGAGATGGCTCTGGGTCCC 690
Db |||||
QY 661 GGGCGGAGTACCGGCTCTGCAGCTGCATCTGCACATGGGGGCTGCAGGTCTGTCGGGC 720
Db |||||
QY 691 GGGCGGAGTACCGGCTCTGCAGCTGCATCTGCACATGGGGGCTGCAGGTCTGTCGGGC 750
Db |||||
QY 721 TCGGAGCACACTGTGGAAGGCCACCGTTTCCCTGCCGAGATCCACGTGTTCACTCAGC 780
Db |||||
QY 751 TCGGAGCACACTGTGGAAGGCCACCGTTTCCCTGCCGAGATCCACGTGTTCACTCAGC 810
Db |||||
QY 781 ACCGCTTTGCCAGAGTTGACGAGGCCCTTGGGGGCCCCGGAGGCCCTGGCCGTGTTGGCC 840
Db |||||
QY 811 ACCGCTTTGCCAGAGTTGACGAGGCCCTTGGGGGCCCCGGAGGCCCTGGCCGTGTTGGCC 870
Db |||||
QY 841 GCCTTTCTGGAGAGGGCCCCGGAAGAAACAGTGCCTATGAGCAGTTGCTGTCTGCTTG 900
Db |||||
QY 871 GCCTTTCTGGAGAGGGCCCCGGAAGAAACAGTGCCTATGAGCAGTTGCTGTCTGCTTG 930
Db |||||
QY 901 GAAGAAATCGTGAAGAGGCTCAGAGACTCAGGTCCAGGACTGGACATATCTGCACCTC 960
Db |||||
QY 931 GAAGAAATCGTGAAGAGGCTCAGAGACTCAGGTCCAGGACTGGACATATCTGCACCTC 990
Db |||||
QY 961 CTGCCCCCTGACTTCAGCCGCTACTTCCAAATGAGGGGTCTCTGACTACACCCGCTGT 1020
Db |||||
QY 991 CTGCCCCCTGACTTCAGCCGCTACTTCCAAATGAGGGGTCTCTGACTACACCCGCTGT 1050
Db |||||
QY 1021 GCCCAGGGTGTCTGAGACTGTGTTTAAACCAGACAGTGTGCTGAGTCTAAGCAGCTC 1080
Db |||||
QY 1051 GCCCAGGGTGTCTGAGACTGTGTTTAAACCAGACAGTGTGCTGAGTCTAAGCAGCTC 1110
Db |||||
QY 1081 CACACCTCTCTGACACCCCTGTGGGACCTGCTGACTCTCGGCTACAGCTGAACCTCCGA 1140
Db |||||
QY 1111 CACACCTCTCTGACACCCCTGTGGGACCTGCTGACTCTCGGCTACAGCTGAACCTCCGA 1170
Db |||||
QY 1141 GCGACGAGCCTTTGAATGGGCGAGTGAATGAGGCTCTCTCCCTGCTGGAGTGGACAGC 1200
Db |||||
QY 1171 GCGACGAGCCTTTGAATGGGCGAGTGAATGAGGCTCTCTCCCTGCTGGAGTGGACAGC 1230
Db |||||
QY 1201 AGTCCTCGGGCTGCTGAGCCAGTCCAGCTGAATTCCTGCTGGTGTGCTGACATCCTA 1260
Db |||||
QY 1231 AGTCCTCGGGCTGCTGAGCCAGTCCAGCTGAATTCCTGCTGGTGTGCTGACATCCTA 1290
Db |||||
QY 1261 GGCCTGTTTTTGGCCTCTTTTGTCTGCTCACCAGCGTCCGCTTCTTTGTGAGATGAGA 1320
Db |||||
QY 1291 GGCCTGTTTTTGGCCTCTTTTGTCTGCTCACCAGCGTCCGCTTCTTTGTGAGATGAGA 1350
Db |||||
QY 1321 AGGACGACAGAAGGGGAACCAAGGGGGTGTGAGTACCAGCCAGCAGAGGTAGCCGAG 1380
Db |||||
QY 1351 AGGACGACAGAAGGGGAACCAAGGGGGTGTGAGTACCAGCCAGCAGAGGTAGCCGAG 1410
Db |||||
QY 1381 ACTGGAGCCTAGAGGCTGGATCTTGGAGATGTGAGAAAGCCAGCCAGAGGCTCTGAGGG 1440
Db |||||
QY 1411 ACTGGAGCCTAGAGGCTGGATCTTGGAGATGTGAGAAAGCCAGCCAGAGGCTCTGAGGG 1470
Db |||||

Db 691 GGGCGGAGTACGGGCTCTGCAGCTGCATCTGCACTGGGGGCTGCAGGTGCTCGGGC 750
Qy 721 TCGGAGCACACTGTGGAAGGCCACCGTTTCCCTGCCGAGATCCACGTGTTCACTCAGC 780
Db 751 TCGGAGCACACTGTGGAAGGCCACCGTTTCCCTGCCGAGATCCACGTGTTCACTCAGC 810
Qy 781 ACCGCCCTTTCAGAGAGTTGACGAGGCTTGGGGCGCCCGGAGGCCTGGCGTGTGGCC 840
Db 811 ACCGCCCTTTCAGAGAGTTGACGAGGCTTGGGGCGCCCGGAGGCCTGGCGTGTGGCC 870
Qy 841 GCCTTTCTGGAGGAGGGCCCGGAAGAAACAGTGCCTATGACAGATTGCTGTCTCGCTG 900
Db 871 GCCTTTCTGGAGGAGGGCCCGGAAGAAACAGTGCCTATGACAGATTGCTGTCTCGCTG 930
Qy 901 GAAGAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCCAGGACTGGACATATCTGCACCTC 960
Db 931 GAAGAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCCAGGACTGGACATATCTGCACCTC 990
Qy 961 CTGCCCTCTGACTTCAGCCGCTACTTCCAATATGAGGGGTCTTGACTACACCGCCCTGT 1020
Db 991 CTGCCCTCTGACTTCAGCCGCTACTTCCAATATGAGGGGTCTTGACTACACCGCCCTGT 1050
Qy 1021 GCCCAGGGTGTCTGGAAGTGTGTTTAAACAGACAGTGTGCTGAGTGTCTAAGCAGCTC 1080
Db 1051 GCCCAGGGTGTCTGGAAGTGTGTTTAAACAGACAGTGTGCTGAGTGTCTAAGCAGCTC 1110
Qy 1081 CACACCCCTCTGACACCCCTGTGGGACCTGGTGACTCTCGGCTACAGCTGAACCTCCGA 1140
Db 1111 CACACCCCTCTGACACCCCTGTGGGACCTGGTGACTCTCGGCTACAGCTGAACCTCCGA 1170
Qy 1141 GCGACGAGCCTTTGAATGGGCGAGTGATTGAGGCCCTCCCTTCCCTGCTGGAGTGGACAGC 1200
Db 1171 GCGACGAGCCTTTGAATGGGCGAGTGATTGAGGCCCTCCCTTCCCTGCTGGAGTGGACAGC 1230
Qy 1201 AGTCTCGGGTGTGAGCCAGTCCAGCTGAATTCCTGCCCTGGCTGCTGGTGACATCCTA 1260
Db 1231 AGTCTCGGGTGTGAGCCAGTCCAGCTGAATTCCTGCCCTGGCTGCTGGTGACATCCTA 1290
Qy 1261 GCCCTGGTTTGGCCCTCCTTTTGTGTACAGCGTGCCTTCCCTTCCCTGCTGGAGTGGAGA 1320
Db 1291 GCCCTGGTTTGGCCCTCCTTTTGTGTACAGCGTGCCTTCCCTTCCCTGCTGGAGTGGAGA 1350
Qy 1321 AGGCAGCACAGAAGGGGAACCAAGGGGTGTGAGCTACCGCCAGCAGAGGTAGCCGAG 1380
Db 1351 AGGCAGCACAGAAGGGGAACCAAGGGGTGTGAGCTACCGCCAGCAGAGGTAGCCGAG 1410
Qy 1381 ACTGGAGCCTAGAGGCTGGATCTTGGAGAAATGTGAGAAAGCCAGCCAGGCACTCAGGG 1440
Db 1411 ACTGGAGCCTAGAGGCTGGATCTTGGAGAAATGTGAGAAAGCCAGCCAGGCACTCAGGG 1470
Qy 1441 GGAGCCGGTAACTGTCTCTGCTCATTATGCCACATTCCTTTTAACTGCCAAGAAATT 1500
Db 1471 GGAGCCGGTAACTGTCTCTGCTCATTATGCCACATTCCTTTTAACTGCCAAGAAATT 1530
Qy 1501 TTTTAAATAAATAATTTATAAT 1522
Db 1531 TTTTAAATAAATAATTTATAAT 1552

RESULT 10
ABX76385

ID ABX76385 standard; DNA; 1552 BP.

XX

AC ABX76385;

XX

DT 02-APR-2003 (first entry)

DE Lung cancer-associated polynucleotide #249.

XX

KW Lung cancer-associated polynucleotide; gene; ds; cytostatic; emphysema;
KW antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;
KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;

KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
KW interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.

XX Unidentified.

PN WO200286443-A2.

XX

PD 31-OCT-2002.

XX

PF 18-APR-2002; 2002WO-US012476.

XX

PR 18-APR-2001; 2001US-0284770P.

PR 10-MAY-2001; 2001US-0290492P.

PR 09-NOV-2001; 2001US-0339245P.

PR 13-NOV-2001; 2001US-0350666P.

PR 29-NOV-2001; 2001US-0334370P.

PR 12-APR-2002; 2002US-0372246P.

XX (EOSB-) EOS BIOTECHNOLOGY INC.

XX Aziz N, Murray R;

PI

XX WPI; 2003-093161/08.

DR P-PSDB; ABU56656.

DR

XX

PT Detecting a lung cancer-associated transcript in a cell from a patient
PT for treating lung cancer, by contacting a biological sample from the
PT patient with a polynucleotide that exhibits increased or decreased
PT expression in lung cancer.

XX

PS Claim 22; Page 379-380; 453pp; English.

XX

CC The invention relates to a method for detecting a lung cancer-associated
CC transcript in a cell from a patient, comprising contacting a biological
CC sample from the patient with a polynucleotide that selectively hybridises
CC to a sequence that is at least 80 % identical to a gene that exhibits
CC increased or decreased expression in lung cancer samples. Lung cancer-
CC associated polynucleotides and polypeptides are used for identifying a
CC compound that modulates a lung cancer-associated polypeptide, for
CC inhibiting proliferation of a lung cancer-associated cell to treat lung
CC cancer in a patient and for treating a mammal having lung cancer by
CC administering a modulatory compound identified. The methods are useful
CC for treating lung cancer, such as small cell lung cancer, non-small cell
CC lung cancer or other benign or precancerous lesions, e.g. atelectasis,
CC emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis,
CC hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and
CC bronchiectasis. The genes, polynucleotides and polypeptides are useful
CC for diagnostic purposes and as targets for screening for therapeutic
CC compounds that modulate lung cancer, such as antibodies. Sequences
CC ABX76124-ABX76474 represent lung cancer-associated polynucleotides of the
CC invention

XX

SQ Sequence 1552 BP; 302 A; 471 C; 461 G; 318 T; 0 U; 0 Other;

Query Match 100.0%; Score 1522; DB 7; Length 1552;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACAGTCAGCGCATGGCTCCCTGTGCCCGCCAGCCCTGGCTCCCTCTGTGATCCCGCC 60

Db 31 ACAGTCAGCGCATGGCTCCCTGTGCCCGCCAGCCCTGGCTCCCTCTGTGATCCCGCC 90

Qy 61 CCTGCTCCAGGCCTCACTGTGCAACTGCTGTCTCACTGTCTTCTGATGCCTGTCCAT 120

Db 91 CCTGCTCCAGGCCTCACTGTGCAACTGCTGTCTCACTGTCTTCTGATGCCTGTCCAT 150

Qy 121 CCCAGAGGTTGCCCGGATGAGGAGGATTCCCGCTTGGAGGAGGCTCTTCTGGGAA 180

Db 151 CCCAGAGGTTGCCCGGATGAGGAGGATTCCCGCTTGGAGGAGGCTCTTCTGGGAA 210

Qy 181 GATGACCCACTGGGCGAGGAGGATCTGCCAGTGAAGAGATTCAACCAGAGGAGGAT 240

Db 211 GATGACCCACTGGGCGAGGAGGATCTGCCAGTGAAGAGATTCAACCAGAGGAGGAT 270

QY 241 CCACCGGAGAGGAGGATCTACTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCT 300
Db 271 CCACCGGAGAGGAGGATCTACTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCT 330
QY 301 GAAGTTAAGCCTAAATCAGAAGAGAGGGCTCCCTGAAGTTAGAGGATCTACCTACTGTT 360
Db 331 GAAGTTAAGCCTAAATCAGAAGAGAGGGCTCCCTGAAGTTAGAGGATCTACCTACTGTT 390
QY 361 GAGGCTCTGGAGATCCTCAAGAACCCAGAAATAATGCCACAGGGACAAAGAAGGGGAT 420
Db 391 GAGGCTCTGGAGATCCTCAAGAACCCAGAAATAATGCCACAGGGACAAAGAAGGGGAT 450
QY 421 GACCAGAGTCATTTGGCGCTATGGAGCGCAGCCCGCCCTGGCCCGGGGTGTCGCCAGCCTGC 480
Db 451 GACCAGAGTCATTTGGCGCTATGGAGCGCAGCCCGCCCTGGCCCGGGGTGTCGCCAGCCTGC 510
QY 481 GCGGGCCGCTTCCAGTCCCCCGGTGGATATCCGCCCCCAGCTCGCCGCTTCTGCCCCGGCC 540
Db 511 GCGGGCCGCTTCCAGTCCCCCGGTGGATATCCGCCCCCAGCTCGCCGCTTCTGCCCCGGCC 570
QY 541 CTGCGCCCCCTGGAACTCCTGGGCTTCCAGCTCCCGCCGCTCCAGAACTGCGCCTGCGC 600
Db 571 CTGCGCCCCCTGGAACTCCTGGGCTTCCAGCTCCCGCCGCTCCAGAACTGCGCCTGCGC 630
QY 601 AACAAATGGCCACAGTGTGCAACTGACCTGCCTCCTGGGCTAGAGATGGCTCTGGGTCCC 660
Db 631 AACAAATGGCCACAGTGTGCAACTGACCTGCCTCCTGGGCTAGAGATGGCTCTGGGTCCC 690
QY 661 GGGCGGGAGTACCGGGCTCTGCAGCTGCATCTGCACCTGGGGGCTGCAGGCTCGTCCGGGC 720
Db 691 GGGCGGGAGTACCGGGCTCTGCAGCTGCATCTGCACCTGGGGGCTGCAGGCTCGTCCGGGC 750
QY 721 TCGGAGCACACTGTGGAAGGCCACCGTTTCCCTGCCGAGATCCACGTGTTCACTCAGC 780
Db 751 TCGGAGCACACTGTGGAAGGCCACCGTTTCCCTGCCGAGATCCACGTGTTCACTCAGC 810
QY 781 ACCGCCCTTGCCAGAGTTGACGAGGCCCTTGGGGCGCCCGGAGGCCCTGGCCGCTGTTGGCC 840
Db 811 ACCGCCCTTGCCAGAGTTGACGAGGCCCTTGGGGCGCCCGGAGGCCCTGGCCGCTGTTGGCC 870
QY 841 GCCTTTCTGAGGAGGGCCCCCGGAAGAAACAGTGCCTATGAGCAGTTGCTGTCTGCTTG 900
Db 871 GCCTTTCTGAGGAGGGCCCCCGGAAGAAACAGTGCCTATGAGCAGTTGCTGTCTGCTTG 930
QY 901 GAAGAAATCGTGTAGGAAGGCTCAGAGACTCAGGTCCAGGACTGGACATATCTGCACTC 960
Db 931 GAAGAAATCGTGTAGGAAGGCTCAGAGACTCAGGTCCAGGACTGGACATATCTGCACTC 990
QY 961 CTGCCCTCTGACTTCAGCCGCTACTTCCAATATGAGGGGTCTTGACTACACCGCCCTGT 1020
Db 991 CTGCCCTCTGACTTCAGCCGCTACTTCCAATATGAGGGGTCTTGACTACACCGCCCTGT 1050
QY 1021 GCCCAGGGTGTATCTGGACTGTGTTTAAACCAGACAGTGTGCTGAGTGTAAAGCAGCTC 1080
Db 1051 GCCCAGGGTGTATCTGGACTGTGTTTAAACCAGACAGTGTGCTGAGTGTAAAGCAGCTC 1110
QY 1081 CACACCCCTCTTGACACCCCTGTGGGGACCTGGTGACTCTCGGCTACAGCTGAATTCGGA 1140
Db 1111 CACACCCCTCTTGACACCCCTGTGGGGACCTGGTGACTCTCGGCTACAGCTGAATTCGGA 1170
QY 1141 GCGACGCAGCCTTTGAATGGGCGAGTGATTTAGGCCCTCTCCCTGCTGGAGTGGACAGC 1200
Db 1171 GCGACGCAGCCTTTGAATGGGCGAGTGATTTAGGCCCTCTCCCTGCTGGAGTGGACAGC 1230
QY 1201 AGTCTCGGGCTGCTGAGCCAGTCCAGCTGAATTCCTGCTGGCTGCTGGTGACATCCTA 1260
Db 1231 AGTCTCGGGCTGCTGAGCCAGTCCAGCTGAATTCCTGCTGGCTGCTGGTGACATCCTA 1290
QY 1261 GCCCTGGTTTTGGCCTCCTTTTGTGTGTCAACGAGTGGGCTTCTTGTGACATGAGA 1320
Db 1291 GCCCTGGTTTTGGCCTCCTTTTGTGTGTCAACGAGTGGGCTTCTTGTGACATGAGA 1350

QY 1321 AGSCAGCACAGAAGGGGAACAAAGGGGGTGTGAGCTACGCCCCAGCAGAGGTAGCCGAG 1380
Db 1351 AGSCAGCACAGAAGGGGAACCAAGGGGGTGTGAGCTACGCCCCAGCAGAGGTAGCCGAG 1410
QY 1381 ACTGGAGCCTAGAGGCTGGATCTTTGGAGAATGTGAGAAGCCAGCCAGAGGCATCTGAGGG 1440
Db 1411 ACTGGAGCCTAGAGGCTGGATCTTTGGAGAATGTGAGAAGCCAGCCAGAGGCATCTGAGGG 1470
QY 1441 GGAGCCGGTAACTGTCTGTCTCTGCTCATTTATGCACTTCTTTTAACTGCCAAGAAATT 1500
Db 1471 GGAGCCGGTAACTGTCTGTCTCTGCTCATTTATGCACTTCTTTTAACTGCCAAGAAATT 1530
QY 1501 TTTTAAATAAATATTATAAT 1522
Db 1531 TTTTAAATAAATATTATAAT 1552
RESULT 11
ABX76124
ID ABX76124 standard; DNA; 1552 BP.
XX
AC ABX76124;
XX
DT 02-APR-2003 (first entry)
XX
DE Lung cancer-associated polynucleotide #1.
KW Lung cancer-associated polynucleotide; gene; ds; cytostatic; emphysema;
antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;
small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
XX
OS Unidentified.
XX
PN WO200286443-A2.
XX
PD 31-OCT-2002.
PF
PF 18-APR-2002; 2002WO-US012476.
XX
PR 18-APR-2001; 2001US-0284770P.
PR 10-MAY-2001; 2001US-0290492P.
PR 09-NOV-2001; 2001US-0339245P.
PR 13-NOV-2001; 2001US-0350666P.
PR 29-NOV-2001; 2001US-0334370P.
PR 12-APR-2002; 2002US-0372246P.
XX
PA (EOSB-) EOS BIOTECHNOLOGY INC.
XX
PI Aziz N, Murray R;
XX
DR WPI; 2003-093161/08.
DR P-PSDB; ABU56408.
XX
PT Detecting a lung cancer-associated transcript in a cell from a patient
for treating lung cancer, by contacting a biological sample from the
patient with a polynucleotide that exhibits increased or decreased
expression in lung cancer.
XX
PS Claim 22; Page 189; 453pp; English.
XX
CC The invention relates to a method for detecting a lung cancer-associated
transcript in a cell from a patient, comprising contacting a biological
sample from the patient with a polynucleotide that selectively hybridises
to a sequence that is at least 80 % identical to a gene that exhibits
increased or decreased expression in lung cancer samples. Lung cancer-
associated polynucleotides and polypeptides are used for identifying a
compound that modulates a lung cancer-associated polypeptide, for
inhibiting proliferation of a lung cancer-associated cell to treat lung
cancer in a patient and for treating a mammal having lung cancer by
administering a modulatory compound identified. The methods are useful
for treating lung cancer, such as small cell lung cancer, non-small cell

CC lung cancer or other benign or precancerous lesions, e.g. atelectasis,
CC emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis,
CC hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and
CC bronchiectasis. The genes, polynucleotides and polypeptides are useful
CC for diagnostic purposes and as targets for screening for therapeutic
CC compounds that modulate lung cancer, such as antibodies. Sequences
CC ABX76124-ABX76474 represent lung cancer-associated polynucleotides of the
XX invention

SQ Sequence 1552 BP; 302 A; 471 C; 461 G; 318 T; 0 U; 0 Other;

Query Match 100.0%; Score 1522; DB 7; Length 1552;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ACAGTCAGCCGCA	TGGCTCCCTGTG	CCCCAGCCCTGGCTCCCTCTGTTGATCCCGGC	60
Db	31	ACAGTCAGCCGCA	TGGCTCCCTGTG	CCCCAGCCCTGGCTCCCTCTGTTGATCCCGGC	90
QY	61	CCTGCTCCAGGC	CTCACTGTGCA	ACTGCTGCTCACTGCTGCTTGTGATGCCCTGCCAT	120
Db	91	CCTGCTCCAGGC	CTCACTGTGCA	ACTGCTGCTCACTGCTGCTTGTGATGCCCTGCCAT	150
QY	121	CCCCAGAGTTG	CCCCGGATG	CAGGAGGATTCCTCCCTTGGGAGGAGGCTCTTCTGGGAA	180
Db	151	CCCCAGAGTTG	CCCCGGATG	CAGGAGGATTCCTCCCTTGGGAGGAGGCTCTTCTGGGAA	210
QY	181	GATGACCCACT	GGCGAGGAGGAT	CTGCCAGTGAAGAGGATTCACCCAGAGAGGAGAT	240
Db	211	GATGACCCACT	GGCGAGGAGGAT	CTGCCAGTGAAGAGGATTCACCCAGAGAGGAGAT	270
QY	241	CCACCCGGAG	GAGGATCTAC	CTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCT	300
Db	271	CCACCCGGAG	GAGGATCTAC	CTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCT	330
QY	301	GAAGTTAAGC	CTAAATCAGA	AGAGGGCTCCCTGAAGTTAGAGGATCTACCTACTGTT	360
Db	331	GAAGTTAAGC	CTAAATCAGA	AGAGGGCTCCCTGAAGTTAGAGGATCTACCTACTGTT	390
QY	361	GAGGCTCCTG	GAGATCCTCA	AGAACCCACAGATTAATGCCCCACAGGGACAAAGAGGGAT	420
Db	391	GAGGCTCCTG	GAGATCCTCA	AGAACCCACAGATTAATGCCCCACAGGGACAAAGAGGGAT	450
QY	421	GACCAGAGTC	ATTGGCGCTAT	TGGAGGGACCCCGCCCTGGCCCGGGTGTCCTCCAGCTGC	480
Db	451	GACCAGAGTC	ATTGGCGCTAT	TGGAGGGACCCCGCCCTGGCCCGGGTGTCCTCCAGCTGC	510
QY	481	GCGGGCCGCT	TCCAGTCCCG	TGGATATCCGCCCCAGCTCGCCGCTTCTGTCGCCGGCC	540
Db	511	GCGGGCCGCT	TCCAGTCCCG	TGGATATATCCGCCCCAGCTCGCCGCTTCTGTCGCCGGCC	570
QY	541	CTGCGCCCCC	TGGAACCTC	TGGCTCCAGCTCCCGCCGCTCCACAGAACTGCGCTGCGC	600
Db	571	CTGCGCCCCC	TGGAACCTC	TGGCTCCAGCTCCCGCCGCTCCACAGAACTGCGCTGCGC	630
QY	601	AACAATGGCC	CACAGTGTG	CAACTGACCCCTGCCTCCTGGGCTAGAGATGGCTCTGGGTCCC	660
Db	631	AACAATGGCC	CACAGTGTG	CAACTGACCCCTGCCTCCTGGGCTAGAGATGGCTCTGGGTCCC	690
QY	661	GGGCGGGAG	TACCGGGCT	CTGCAGCTGCATCTGCACCTGGGGGGCTGCAGGTCTCCGGGC	720
Db	691	GGGCGGGAG	TACCGGGCT	CTGCAGCTGCATCTGCACCTGGGGGGCTGCAGGTCTCCGGGC	750
QY	721	TCGGAGCAC	ACTGTGGA	AGGCCACCGTTTCCCTGCCGAGATCCACGTGGTTACCTCAGC	780
Db	751	TCGGAGCAC	ACTGTGGA	AGGCCACCGTTTCCCTGCCGAGATCCACGTGGTTACCTCAGC	810
QY	781	ACCGCCTTT	GCCACAGTT	GACGAGGCTTGGGGCGCCCGGGAGGCTTGGCCGTTGGGCC	840
Db	811	ACCGCCTTT	GCCACAGTT	GACGAGGCTTGGGGCGCCCGGGAGGCTTGGCCGTTGGGCC	870
QY	841	GCCTTTCTG	GAGGAGGGCC	CGGAAGAAACAGTGCCTATGAGCAGTTGCTGCTCGCTTG	900

Db	871	GCCTTTCTG	AGGAGGGCCC	CGGAAGAAAC	AGTGCCTATGAGCAGTTGCTGTCTCGCTTG	930
QY	901	GAAGAAATC	GCTGAGGA	AGGCTCAG	AGACTCAGGTCCCAGGACTGGACATATCTGCATC	960
Db	931	GAAGAAATC	GCTGAGGA	AGGCTCAG	AGACTCAGGTCCCAGGACTGGACATATCTGCATC	990
QY	961	CTGCCCTCT	GACTTCAG	CCCGCTACT	TCCAATATGAGGGGTCTCTGACTACACCCCTGT	1020
Db	991	CTGCCCTCT	GACTTCAG	CCCGCTACT	TCCAATATGAGGGGTCTCTGACTACACCCCTGT	1050
QY	1021	GCCCAGG	GTGCATCT	GGA	CTGTGTTTAAACCAGACAGTATGCTGAGTCTAAGCAGCTC	1080
Db	1051	GCCCAGG	GTGCATCT	GGA	CTGTGTTTAAACCAGACAGTATGCTGAGTCTAAGCAGCTC	1110
QY	1081	CACACCC	CTCTTG	ACACCCCTGTGGG	ACCTGGTGACTCTCGGCTACAGCTGAACCTTCCGA	1140
Db	1111	CACACCC	CTCTTG	ACACCCCTGTGGG	ACCTGGTGACTCTCGGCTACAGCTGAACCTTCCGA	1170
QY	1141	GCGACGC	AGCCTTT	GAA	TGGCGAGTGATGAGGCCCTCTTCCCTGCTGGAGTGACAGC	1200
Db	1171	GCGACGC	AGCCTTT	GAA	TGGCGAGTGATGAGGCCCTCTTCCCTGCTGGAGTGACAGC	1230
QY	1201	AGTCTCG	GGCTGCT	GAGCCAGT	CCAGCTGAATTCCTGCCCTGGTGGTGCATCCTA	1260
Db	1231	AGTCTCG	GGCTGCT	GAGCCAGT	CCAGCTGAATTCCTGCCCTGGTGGTGCATCCTA	1290
QY	1261	GCCCTGG	TTTTTGG	CCTCCTTTT	TGCTGTCCAGCGTCCCTTGTGCAGATGAGA	1320
Db	1291	GCCCTGG	TTTTTGG	CCTCCTTTT	TGCTGTCCAGCGTCCCTTGTGCAGATGAGA	1350
QY	1321	AGGCAGC	ACAGAA	GGGGAACCA	AAAGGGGTGTGAGCTACCGCCACAGAGGTAGCCGAG	1380
Db	1351	AGGCAGC	ACAGAA	GGGGAACCA	AAAGGGGTGTGAGCTACCGCCACAGAGGTAGCCGAG	1410
QY	1381	ACTGGAG	CCCTAG	AGGCTGGAT	CTTGGAGAAATGTGAGAAAGCCAGAGGCATCTGAGGG	1440
Db	1411	ACTGGAG	CCCTAG	AGGCTGGAT	CTTGGAGAAATGTGAGAAAGCCAGAGGCATCTGAGGG	1470
QY	1441	GGAGCCG	GTA	ACTGTCTGT	CCTCATTTATGCCACTTCTTTAACTGCCAAGAAAT	1500
Db	1471	GGAGCCG	GTA	ACTGTCTGT	CCTCATTTATGCCACTTCTTTAACTGCCAAGAAAT	1530
QY	1501	TTTTTAA	ATAA	TATTTATA	TAT 1522	
Db	1531	TTTTTAA	ATAA	TATTTATA	TAT 1552	

RESULT 12

AAH26551	ID	AAH26551	standard; cDNA; 1833 BP.
XX	XX	AAH26551;	
AC	AC		
XX	XX		
DT	DT	12-NOV-2001	(first entry)
XX	XX		
DE	DE	DNA encoding G250-GM-CSF fusion protein.	
XX	XX		
KW	KW	GM-CSF; granulocyte-macrophage colony stimulating factor; G250; vaccine; genetic immunisation; adoptive immunotherapy; therapy; kidney cancer; antigen; renal cell carcinoma; tumour; human; gene therapy; antitumour; ss.	
KW	KW		
XX	XX		
OS	OS	Homo sapiens.	
OS	OS	Synthetic.	
XX	XX		
FH	FH	Key	Location/Qualifiers
CDS	CDS	1..1815	
FT	FT	/*tag= a	
FT	FT	/product= "G250-GM-CSF"	
FT	FT	/transl_except= (pos:433..435, aa:Arg)	
FT	FT	/transl_except= (pos:436..438, aa:Arg)	
XX	XX		
PN	PN	WO200160317-A2.	

XX MN cDNA clone.
DE MN; endogenous; MaTu; quasi-viral agent; human; mammary tumour;
XX classical virus; slow virus; prion; exogenous MX; p58X;
KW cytoplasmic antigen; conservative; HeLa cell; twin protein; p54/58N;
KW cell surface; nucleus; monoclonal antibody; MAb M75; neoplasm;
KW pre-neoplastic disease; vaccine; ss.

XX Homo sapiens.

XX Key Location/Qualifiers
FT CDS 1..1290
FT /*tag= a

PN WO9318152-A1.
XX 16-SEP-1993.
XX 08-MAR-1993; 93WO-US002024.
XX 11-MAR-1992; 92CS-00000709.
PR 21-OCT-1992; 92US-00964589.

XX (CIBA) CIBA CORNING DIAGNOSTICS CORP.
PA (VIRO-) INST VIROLOGY.

PI Zavada J, Pastorekova S, Pastorek J;
XX WPI; 1993-303466/38.
DR P-PSDB; AAR41746.

XX New MN gene and polypeptide(s) - used in diagnosis, prognosis and therapy
PT of neoplastic and/or pre-neoplastic disease.

XX Claim 2; Fig 1; 72pp; English.

CC This sequence represents the intronless MN gene which is a cellular gene
CC which is the endogenous component of the MaTu agent. MaTu is a novel
CC quasi-viral agent with rather unusual properties. It is presumably
CC derived from a human mammary tumour. In some aspects it resembles
CC classical viruses, whereas in other respects it resembles "slow" viruses
CC (prions), and in still other aspects it is different from both classes of
CC viruses. MaTu is a two component sytem. One part of the complex,
CC exogenous MX, is transmissible, and is manifest by a protein, p58X, which
CC is a cytoplasmic antigen which reacts with some natural sera, of humans
CC and of various animals. The other component, MN, is endogenous to human
CC cells. MN is a cellular gene showing very little homology with known DNA
CC sequences. It is rather conservative and present as a single copy in the
CC chromosomal DNA of various vertebrates. MN is manifest in HeLa cells by a
CC twin protein p54/58N, that is localised on the cell surface and in the
CC nucleus. Immunoblots using a monoclonal antibody reactive with p54/58N
CC (Mab M75) reveals two bands at 54 kD and 58 kD. These two bands may
CC correspond to one type of protein that differs by glycosylation pattern
CC or by how it is processed. The expression of the MN gene is strongly
CC correlated with tumourigenicity. MN products can be used in can be used
CC in diagnostic and/or prognostic assays for neoplastic and/or pre-
CC neoplastic disease. MN polypeptides, produced recombinantly by
CC unicellular hosts, can also be used for antibody production and in
CC vaccines for inducing protective immunity against neoplastic disease and
CC a dampening effect upon tumourigenic activity. (Updated on 25-MAR-2003 to
CC correct PN field.)

XX Sequence 1397 BP; 284 A; 402 C; 425 G; 286 T; 0 U; 0 Other;
SQ
Query Match 85.6%; Score 1302.8; DB 2; Length 1397;
Best Local Similarity 99.3%; Pred. No. 1.2e-307;
Matches 1392; Conservative 0; Mismatches 2; Indels 8; Gaps 8;

QY 124 CAGAGGTTGCCCCGGATGCAGGAGGATCCCCCTTGGGAGGAGGCTCTTCTGGGGAAGAT 183
DB |
1 CAGAGGTTGCCCCGGATGCAGGAGGATCCCCCTT-GGAGGAGGCTCTTCTGGGGAAGAT 59

QY 184 GACCCACTGGCGAGGAGGATCTGCCAGTGAAGAGGATTCACCAGAGAGGAGGATCCA 243
DB |||||
60 GACCCACTGGCGAGGAGGATCTGCCAGTGAAGAGGATTCACCAGAGAGGAGGATCCA 119
QY 244 CCGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGAA 303
DB |||||
120 CCGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGAA 179
QY 304 GTTAA-GCCTAAATCAGAAGAAGAGGGCTCCCTGAAGTTAGAGGATCTACCTACTGTTGA 362
DB |||||
180 GTTAATGCCCTAAATCAGAAGAAGAGGGCTCCCTGAAGTTAGAGGATCTACCTACTGTTGA 239
QY 363 GGCTCCTGGAGATCCTCAAGAACCCAGAAATAATGCCACAGGGACAAAGAAGGGGATGA 422
DB |||||
240 GGCTCCTGGAGATCCTCAAGAACCCAGAAATAATGCCACAGGGACAAAGAAGGGGATGA 299
QY 423 CCAGAGTCAATTGGCGCTATGGAGGGACCCCGCTGGCCCGGGTGTCCCAGCCTGCGC 482
DB |||||
300 CCAGAGTCAATTGGCGCTATGGAGGGACCCG-CCTGGCCCGGGTGTCCCAGCCTGCGC 358
QY 483 GGGCCGCTTCCAGTCCCGGTGGATATCCGCCCCCCAGCTCGCGCTTCTGCCCGGCCCT 542
DB |||||
359 GGGCCGCTTCCAGTCCCGGTGGATATCCGCCCCCCAGCTCGCGCTTCTGCCCGGCCCT 418
QY 543 GCGCCCCCTGGAATCCTGGGCTTCCAGCTCCCGCCGCTCCAGAACTGCGCTGCGCAA 602
DB |||||
419 GCGCCCCCTGGAATCCTGGGCTTCCAGCTCCCGCCGCTCCAGAACTGCGCTGCGCAA 477
QY 603 CAATGGCCACAGTGTGCAACTGACCTGCCTCCTGGGCTAGAGATGGCTCTGGGTCCCGG 662
DB |||||
478 CAATGGCCACAGTGTGCAACTGACCTGCCTCCTGGGCTAGAGATGGCTCTGGGTCCCGG 537
QY 663 GCGGAGTACCGGGCTCTGCAGTGCATCTGCATGGGGGGTGCAGGTCTGTCGGGCTC 722
DB |||||
538 GCGGAGTACC-GGCTCTGCAGTGCATCTGCATGGGGGGTGCAGGTCTGTCGGGCTC 596
QY 723 GGAGCACACTGTGGAAGGCCACCGTTTCCCTGCCGAGATCCAGTGGTTCACTCAGCAC 782
DB |||||
597 GGAGCACACTGTGGAAGGCCACCGTTTCCCTGCCGAGATCCAGTGGTTCACTCAGCAC 656
QY 783 CGCCTTTGCCAGAGTTGACGAGGCTTGGGGCGCCCGGAGGCTGGCCGTGTTGGCCGC 842
DB |||||
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QY 843 CTTTCTGGAGAGGGCCCGGAAGAAAACAGTG-CCTATGAGCAGTTGCTGTCTCGCTTGG 901
DB |||||
716 CTTTCTGGAGAGGGCCCGGAAGAAAACAGTGCTCTATGAGCAGTTGCTGTCTCGCTTGG 775
QY 902 AAGAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCCAGGACTGGACATATCTGCACCTC 961
DB |||||
776 AAGAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCCAGGACTGGACATATCTGCACCTC 835
QY 962 TGCCCTCTGACTTCAAGCGCTACTTCCAATATGAGGGGTCTCTGACTACACCGCCCTGTG 1021
DB |||||
836 TGCCCTCTGACTTCAAGCGCTACTTCCAATATGAGGGGTCTCTGACTACACCGCCCTGTG 895
QY 1022 CCAGGGTGTCTGACTGTGTGTTTAAACAGACAGTGTGCTGAGTGTGCTAAGCAGCTCC 1081
DB |||||
896 CCCAGGGTGTCTGACTGTGTGTTTAAACAGACAGTGTGCTGAGTGTGCTAAGCAGCTCC 955
QY 1082 ACACCCCTCTGACACCCCTGTGGGGACCTGGTGACTCTCGGCTACAGCTGAACCTCCGAG 1141
DB |||||
956 ACACCCCTCTGACACCCCTGTGGGGACCTGGTGACTCTCGGCTACAGCTGAACCTCCGAG 1015
QY 1142 CGACGCAGCCTTTGAATGGGGCAGTGAATTGAGGCCCTCCTTCCCTGCTGGAGTGACAGCA 1201
DB |||||
1016 CGACGCAGCCTTTGAATGGGGCAGTGAATTGAGGCCCTCCTTCCCTGCTGGAGTGACAGCA 1075
QY 1202 GTCTCTGGGCTGCTGAGCCAGTCCAGCTGAATTCCTGCTGGCTGCTGGTACATCCTAG 1261
DB |||||
1076 GTCTCTGGGCTGCTGAGCCAGTCCAGCTGAATTCCTGCTGGCTGCTGGTACATCCTAG 1135
QY 1262 CCCTGGTTTTTTGGCCCTCCTTTTTTGTGCTCACCAGCGTCGCGTTCCTTGTGAGATGAGAA 1321

Db 1136 CCCTGGTTTGGCTCCTTTTGTGCTGTCAACGCGTGGCTTCTTGTGAGATGAGAA 1195
QY 1322 GGCAGCACAGAGGGGAACCAAGGGGTGTGAGC-TACCGCCCAGCAGAGGTAGCCGAG 1380
Db 1196 GGCAGCACAGAGGGGAACCAAGGGGTGTGAGCGTACCGCCCAGCAGAGGTAGCCGAG 1255
QY 1381 ACTGGAGCCTAGAGGCTGGATCTTGGAGAATGTGAGAAGCCAGCCAGAGGCATCTGAGGG 1440
Db 1256 ACTGGAGCCTAGAGGCTGGATCTTGGAGAATGTGAGAAGCCAGCCAGAGGCATCTGAGGG 1315
QY 1441 GGAGCCGGTAACGTCTGTCTGTCTCATTATGCCACTTCTTTTAAGTCCAAAGAAATT 1500
Db 1316 GGAGCCGGTAACGTCTGTCTGTCTCATTATGCCACTTCTTTTAAGTCCAAAGAAATT 1375
QY 1501 TTTTAAAAATAAATATTTATAAT 1522
Db 1376 TTTTAAAAATAAATATTTATAAT 1397

RESULT 14
ADB53977
ID ADB53977 standard; DNA; 6521 BP.
XX
AC ADB53977;
XX
DT 04-DEC-2003 (first entry)
XX
DE MNCA9 genomic DNA region.
XX
KW colon cell proliferative disorder; non methylated CpG dinucleotide;
KW cytosstatic; cancer; adenoma; carcinoma; cytosine methylation state; ds.
XX
OS Unidentified.
XX
PN WO2003072821-A2.
XX
PD 04-SEP-2003.
XX
PF 27-FEB-2003; 2003WO-EP002035.
XX
PR 27-FEB-2002; 2002EP-00004551.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Adorjan P, Burger M, Maier S, Nimmrich I, Becker E, Lesche R;
PI Rujan T, Schmitt A;
XX
DR WPI; 2003-731620/69.

XX
PT Detecting and differentiating between colon cell proliferative disorders
PT associated with a gene or its regulatory regions comprises contacting a
PT target nucleic acid in a biological sample obtained from the subject with
PT a reagent.
XX
PS Claim 46; SEQ ID NO 33; 74pp; English.
XX
CC The invention relates to a novel method for detecting and differentiating
CC between colon cell proliferative disorders associated with at least one
CC gene or its regulatory regions. The method comprises contacting a target
CC nucleic acid in a biological sample obtained from the subject with at
CC least one reagent or a series of reagents, where the reagent or series of
CC reagents, distinguishes between methylated and non methylated CpG
CC dinucleotides within the target nucleic acid. The molecules of the
CC invention demonstrate cytostatic activity whilst the method may useful
CC for detecting and differentiating between colon cell proliferative
CC disorders, including cancers such as colon adenoma and colon carcinoma.
CC The PNA (peptide nucleic acid)-oligomers are useful as probes for
CC determining cytosine methylation state or single nucleotide
CC polymorphisms. The current sequence is that of the genomic DNA region of
CC the invention. This sequence is not shown within the specification but is
CC taken from Wipoweb.
XX

SQ Sequence 6521 BP; 1650 A; 1570 C; 1641 G; 1660 T; 0 U; 0 Other;
Query Match 27.2%; Score 414.4; DB 9; Length 6521;
Best Local Similarity 99.8%; Pred. No. 1.2e-90;
Matches 415; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ACAGTCAGCCGCATGGCTCCCTGTGCCCCAGCCCTGGCTCCCTCTGTGATCCCGGCC 60
Db 4931 ACAGTCAGCCGCATGGCTCCCTGTGCCCCAGCCCTGGCTCCCTCTGTGATCCCGGCC 4990
QY 61 CCTGCTCCAGGCCCTCACTGTGCAACTGCTGTCTGCTCACTGTCTTCTGATGCCTGTCCAT 120
Db 4991 CCTGCTCCAGGCCCTCACTGTGCAACTGCTGTCTGCTCACTGTCTTCTGCTGCTGTCCAT 5050
QY 121 CCCACAGGTTGCCCGGATGCAGGAGGATTCCCCCTTGGGAGGAGGCTCTTCTGGGGAA 180
Db 5051 CCCACAGGTTGCCCGGATGCAGGAGGATTCCCCCTTGGGAGGAGGCTCTTCTGGGGAA 5110
QY 181 GATGACCCACTGGGCGAGGAGGATCTGCCCAGTGAAGAGGATTCACCCAGAGAGGAGGAT 240
Db 5111 GATGACCCACTGGGCGAGGAGGATCTGCCCAGTGAAGAGGATTCACCCAGAGAGGAGGAT 5170
QY 241 CCACCCGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCT 300
Db 5171 CCACCCGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCT 5230
QY 301 GAAGTTAAGCCTAAATCAGAAGAAGAGGGCTCCCTGAAAGTTAGAGGATCTACCTACTGTT 360
Db 5231 GAAGTTAAGCCTAAATCAGAAGAAGAGGGCTCCCTGAAAGTTAGAGGATCTACCTACTGTT 5290
QY 361 GAGGCTCCTGGAGATCCTCAAGAACCCCAAGATAATGCCCCACAGGGACAAAGAAGG 416
Db 5291 GAGGCTCCTGGAGATCCTCAAGAACCCCAAGATAATGCCCCACAGGGACAAAGAAGG 5346

RESULT 15
AAT09187
ID AAT09187 standard; DNA; 10897 BP.
XX
AC AAT09187;
XX
DT 25-MAR-2003 (revised)
DT 26-JUL-1996 (first entry)
XX
DE MuTu putative oncogene MN genomic DNA.
XX
KW MuTu; endogenous; cellular component; MN; HeLa cell; diagnosis;
KW lymphocytic choriomeningitis virus; LCMV; putative oncogene; treatment;
KW neoplastic; pre-neoplastic; disease; antisense therapy; antibody;
KW vaccine; vertebrate; immunisation; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT misc_feature 1973
FT /tag= a
FT /note= "given as "?" in specification"
FT exon 3536..3950
FT /tag= b
FT /number= 1
FT exon 5125..5154
FT /tag= c
FT /number= 2
FT exon 5350..5518
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FT exon 10561. .10751
FT /*tag= l
FT /number= 11
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XX
PN W09534650-A2.
XX
PD 21-DEC-1995.
XX
XX 15-JUN-1995; 95WO-US007628.
XX
PR 15-JUN-1994; 94US-00260190.
PR 07-JUN-1995; 95US-00477504.
PR 07-JUN-1995; 95US-00481658.
PR 07-JUN-1995; 95US-00485049.
PR 07-JUN-1995; 95US-00485862.
PR 07-JUN-1995; 95US-00485863.
PR 07-JUN-1995; 95US-00486756.
PR 07-JUN-1995; 95US-00487077.
XX

(CIBA) CIBA CORNING DIAGNOSTICS CORP.
(VIRO-) INST VIROLOGY.

Zavada J, Pastorekova S, Pastorek J;

WPI; 1996-049679/05.

MN gene, protein and nucleic acid fragments - used as primers and probes in the detection of MN antigens and antibodies, and in the treatment of (pre)neoplastic disease.

Claim 1; Fig 3; 102pp; English.

The present sequence is the complete MuTu endogenous cellular component, MN, genomic DNA, which was isolated from lymphocytic choriomeningitis virus (LCMV) infected HeLa cells. Persistent LCMV, the exogenous MuTu transmissible agent (MX), infection increases the expression level of the MN gene. MN is a putative oncogene, and can therefore be used in the development of prods. for the diagnosis and treatment of neoplastic (NP), or pre-NP diseases. NP diseases can be treated using DNA antisense to MN transcribed mRNA, anti-MN protein antibodies can be used for the diagnosis NP or pre-NP diseases and a vaccine contg. immunogenic amounts of the MN protein can be used to immunise a vertebrate against a NP disease associated with MN antigen expression. (Updated on 25-MAR-2003 to correct PR field.)

Sequence 10897 BP; 2654 A; 2738 C; 2647 G; 2857 T; 0 U; 1 Other;

Query Match 27.2%; Score 414.4; DB 2; Length 10897;
Best Local Similarity 99.8%; Pred. No. 1.4e-90;
Matches 415; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACAGTCAGCCGCGCATGGCTCCCTGTGCCCCAGCCCCCTGGCTCCCTCTGTTGATCCCGGCC 60
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
3536 ACAGTCAGCCGCGCATGGCTCCCTGTGCCCCAGCCCCCTGGCTCCCTCTGTTGATCCCGGCC 3595
QY 61 CCTGCTCCAGGCCTCACTGTGCAACTGCTGCTGTCACTGCTGCTTCTGATGCCGTGTCCAT 120
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
3596 CCTGCTCCAGGCCTCACTGTGCAACTGCTGCTGTCACTGCTGCTTCTGTCCTGTTCAT 3655

QY 121 CCCCAGAGGTTGCCCGGATGCAGGAGGATTCCCCCTTGGGAGGAGGCTCTTCTGGGGAA 180
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
3656 CCCCAGAGGTTGCCCGGATGCAGGAGGATTCCCCCTTGGGAGGAGGCTCTTCTGGGGAA 3715
QY 181 GATGACCCCACTGGGCGAGGAGGATCTGCCAGTGAAGAGGATTCAACCAGAGAGGAGGAT 240
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
3716 GATGACCCCACTGGGCGAGGAGGATCTGCCAGTGAAGAGGATTCAACCAGAGAGGAGGAT 3775
QY 241 CCACCCGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCT 300
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
3776 CCACCCGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCT 3835
QY 301 GAAGTTAAGCCTAAATCAGAAAGAAAGAGGGGCTCCCTGAAGTTAGAGGATCTACCTACTGTT 360
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
3836 GAAGTTAAGCCTAAATCAGAAAGAAAGAGGGGCTCCCTGAAGTTAGAGGATCTACCTACTGTT 3895
QY 361 GAGGCTCCTGGAGATCCTCAAGAACCCCAAGATAATGCCCAACAGGGACAAAGAAGG 416
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
3896 GAGGCTCCTGGAGATCCTCAAGAACCCCAAGATAATGCCCAACAGGGACAAAGAAGG 3951

Search completed: May 11, 2004, 13:44:50
Job time : 648 secs

GenCore version 5.1.6
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OMnucleic - nucleic search, using sw model

Run on: May 11, 2004, 12:29:03 ; Search time 4181 Seconds
(without alignments)
10870.662 Million cell updates/sec

Title: US-09-807-949B-1
Perfect score: 1522
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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5: em_estov:*
6: em_estpl:*
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8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
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16: em_estom:*
17: em_gss_hum:*
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22: em_gss_mam:*
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27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	DB ID	Description
1	1053.8	69.2	1201	9	AL542336
2	920.8	60.5	1201	9	AL554705
3	915	60.1	1013	13	BX423970
4	903.4	59.4	1072	9	AL558378

C	5	865.2	56.8	1201	9	AL554665	AL554665
C	6	832	54.7	1201	13	BX401186	BX401186
C	7	813.6	52.4	1007	13	BX423969	BX423969
C	8	796.8	52.4	1031	9	AL577748	AL577748
C	9	789.4	51.9	1017	9	AL580216	AL580216
C	10	772.6	50.8	1067	9	AL555184	AL555184
C	11	731.4	48.1	874	12	BG386425	BG386425
C	12	669.8	44.0	689	14	CA425935	CA425935
C	13	665.8	43.7	682	9	AI831707	AI831707
C	14	665.4	43.7	1074	13	BX383092	BX383092
C	15	660.4	43.4	691	13	BU620600	BU620600
C	16	650.6	42.7	795	9	AW083955	AW083955
C	17	647	42.5	669	9	AI925646	AI925646
C	18	644	42.3	668	12	BG824243	BG824243
C	19	629.2	41.3	733	12	BG819731	BG819731
C	20	627.8	41.2	658	9	AI769526	AI769526
C	21	625.6	41.1	818	10	BE548062	BE548062
C	22	620.8	40.8	806	10	BF344769	BF344769
C	23	608.4	40.0	659	14	CA416326	CA416326
C	24	586.4	38.5	589	12	BM790508	BM790508
C	25	582.2	38.3	618	10	AW615291	AW615291
C	26	575.6	37.8	814	9	AI241681	AI241681
C	27	572	37.6	627	12	BM552941	BM552941
C	28	569.8	37.4	746	12	BI223232	BI223232
C	29	564	37.1	577	9	AI032380	AI032380
C	30	541.6	35.6	736	10	BE543633	BE543633
C	31	522.6	34.3	581	9	AI023541	AI023541
C	32	514.6	33.8	543	9	AA879425	AA879425
C	33	512	33.6	579	9	AI400286	AI400286
C	34	501.2	32.9	525	9	AI979142	AI979142
C	35	495.8	32.6	551	14	CA406362	CA406362
C	36	489	32.1	489	9	AI791726	AI791726
C	37	488.2	32.1	969	13	BX370540	BX370540
C	38	474.2	31.2	945	14	CF579370	CF579370
C	39	465.2	30.6	717	10	AW701559	AW701559
C	40	461	30.3	541	12	BM792326	BM792326
C	41	456.8	30.0	597	12	BG746869	BG746869
C	42	450.8	29.6	649	13	BY735107	BY735107
C	43	448.6	29.5	610	14	CF177855	CF177855
C	44	447.8	29.4	465	10	AW293135	AW293135
C	45	424	27.9	438	10	AW449513	AW449513

ALIGNMENTS

RESULT 1	AL542336	AL542336	1201 bp	mRNA	linear	EST 12-MAY-2003
LOCUS	AL542336	Homo sapiens PLACENTA	Homo sapiens	cdna	clone	CS0DE010YB19
DEFINITION	5-PRIME, mRNA	sequence.				
ACCESSION	AL542336					
VERSION	AL542336.2	GI:30547384				
KEYWORDS	EST.					
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
AUTHORS	Li, W.B., Gruber, C., Jessee, J. and Polayes, D.					
TITLE	Full-length cDNA libraries and normalization					
JOURNAL	Unpublished (2001)					
COMMENT	On Feb 15, 2001 this sequence version replaced gi:12874280. Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 8734.f For more information about this cluster, see http://www.genoscope.cns.fr/ cgi-bin/cluster.cgi?seq=CS0DE010CA10QP2&cluster=8734.f. Contact : Feng Liang Email : fliang@lifetech.com URL :					

http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DE010CA10QP2.
FEATURES
Location/Qualifiers
source
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DE010YB19"
/tissue type="PLACENTA"
/clone_lib="Homo sapiens PLACENTA"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."

ORIGIN
Query Match 69.2%; Score 1053.8; DB 9; Length 1201;
Best Local Similarity 96.2%; Pred. No. 3.7e-224;
Matches 1086; Conservative 21; Mismatches 19; Indels 3; Gaps 3;

Qy 1 ACAGTCAGCCGATGGCTCCCTGTGCCCCAGCCCTGGCTCCCTCTGTTGATCCCGGCC 60
Db
75 ACAGTCAGCCGATGS-TCCCTGTGCCCCAGCCCTGGCTCCCTCTGTTGATCCCGGCC 133

Qy 61 CTGCTCCAGGCCTCACTGTGCAACTGCTGTGCTCACTGCTGCTTCTGATGCCTGTCCAT 120
Db 134 CTGCTCCAGGCCTCACTGTGCAACTGCTGTGCTCACTGCTGCTTCTGGTGCCTGTCCAT 193

Qy 121 CCCAGAGGTTGCCCGGATGCAGGAGGATTCCCCCTTGGGAGGAGGCTTCTTCTGGGAA 180
Db 194 CCCAGAGGTTGCCCGGATGCAGGAGGATTCCCCCTTGGGAGGAGGCTTCTTCTGGGAA 253

Qy 181 GATGACCCACTGGCGGAGGAGGATCTGCCCACTGAAGAGGATTCAACCAGAGAGGAGAT 240
Db 254 GATGACCCACTGGCGGAGGAGGATCTGCCCACTGAAGAGGATTCAACCAGAGAGGAGAT 313

Qy 241 CCACCCGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCT 300
Db 314 CCACCCGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCT 373

Qy 301 GAAGTTAAGCCTAAATCAGAAGAAGAGGGCTCCCTGAAGTTAGAGGATCTACCTACTGTT 360
Db 374 GAAGTTAAGCCTAAATCAGAAGAAGAGGGCTCCCTGAAGTTAGAGGATCTACCTACTGTT 433

Qy 361 GAGGTCCTGGAGATCCTCAAGAACCCAGAAATATGCCACAGGGACAAAGAGGGAT 420
Db 434 GAGGTCCTGGAGATCCTCAAGAACCCAGAAATATGCCACAGGGACAAAGAGGGAT 493

Qy 421 GACCAGAGTCATTGGCGCTATGGAGGGGACCCGCGCTGGCCCGGGTGTCCTCCAGCCTGC 480
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Qy 481 GCGGCGCGCTTCCAGTCCCGGTGGATATCCGCCCCCAGCTCGCCGCTTCTGCCCCGCC 540
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Qy 541 CTGCGCCCCCTGGAACTCCTGGGCTTCCAGCTCCCGCGCTCCAGAACTGGCGCTGCGC 600
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Qy 721 TCGGAGCACACTGTGGAAGGCCACCGTTTCCCTGCCGAGATCCACGTGTTACCTCAGC 780
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781 ACCGCTTTGCCAGAGTTGACGAGGCTTGGGGCGCCCCGGGAGGCGCTGGCCGTGTTGGCC 840
Db
854 ACCGCTTTGCCAGAGTTGACGAGGCTTGGGGCGCCCCGGGAGGCGCTGGCCGTGTTGGCC 913

Qy 841 GCCTTTCTGGAGAGGGCCCGGAAGAAAAACAGTGCCTATGAGCAGTGTGCTCGCTTG 900
Db 914 GCCTTTCTGGAGAGGGCCCGGAAGAAAAACAGTGCCTATGAGCAGTGTGCTCGCTTG 973

Qy 901 GAAGAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCCAGGAC-TGGACATATCTGCAC 959
Db 974 GAAGAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCCAGGACTTGGACATATCTKSAC 1033

Qy 960 CTTGCCCTCTGACTTCAGCCGCTACTTCCAATATGAGGGGTCTCTGACTACACCGCCCTG 1019
Db 1034 CTTGSCCTCTGACTTCAGCCGCTACTTCAAATATGAGGGGCTCTGACTACACCGCCCTG 1093

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Db 1094 TKGCCAGGGTGTCTATCTKGACTGTGTTAAACAGAMAGTKRTTYGTGAGTGTAAAGMRC 1153

Qy 1080 CCACACCCCTCTCTGACACCCCTGTGGGACCTGGTGAAGTCTCGGCTACAG 1128
Db 1154 CCACACCC-YYTGTACACCCCTGTGGGGGCTGGKGRHTTYTGGGTAAAG 1201

RESULT 2
AL554705
LOCUS
DEFINITION AL554705 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0DI085YF18 5-PRIME, mRNA sequence.
ACCESSION AL554705
VERSION AL554705.2 GI:31276515
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Li,W.B., Gruber,C., Jesse,J. and Polayes,D.
AUTHORS Full-length cDNA libraries and normalization
TITLE Unpublished (2001)
JOURNAL On Feb 15, 2001 this sequence version replaced gi:12895743.
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5300.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DI085DC09QP1&cluster=5300.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DI085DC09QP1.
FEATURES
Location/Qualifiers
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/clone="CS0DI085YF18"
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/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Query Match 60.5%; Score 920.8; DB 9; Length 1201;
Best Local Similarity 96.4%; Pred. No. 1.8e-194;
Matches 991; Conservative 13; Mismatches 15; Indels 9; Gaps 6;

Qy 1 ACAGTCAGCCGATGGCTCCCTGTGTCGCCAGCCCTGGCTCCCTCTGTTGATCCCGGCC 60

||||| 99 ACAGTCAGCCGATGGCTCCCTGTGCCCCAGCCCTGGCTCCCTCTGTTGATCCCGGCC 158
QY 61 CCTGCTCAGGCCTCACTGTGCAACTGCTGCTGTCACTGCTGTTCTGATGCCTGTCCAT 120
Db 159 CCTGCTCAGGCCTCACTGTGCAACTGCTGCTGTCACTGCTGTTCTGTTGCCTGTCCAT 218
QY 121 CCCCAGAGGTTGCCCGGATGCAGGAGGATCCCCCTTGGGAGGAGCTCTTCTGGGAA 180
Db 219 CCCCAGAGGTTGCCCGGATGCAGGAGGATCCCCCTTGGGAGGAGCTCTTCTGGGAA 278
QY 181 GATGACCCACTGGCGGAGGAGGATCTGCCAGTGAAGAGGATTCAACCAGAGAGGAGAT 240
Db 279 GATGACCCACTGGCGGAGGAGGATCTGCCAGTGAAGAGGATTCAACCAGAGAGGAGAT 338
QY 241 CCACCCGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCT 300
Db 339 CCACCCGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCT 398
QY 301 GAAGTTAAGCCTAAATCAGAAGAACAGAGGCTCCCTGAAGTTAGAGGATCTACCTACTGTT 360
Db 399 GAAGTTAAGCCTAAATCAGAAGAACAGAGGCTCCCTGAAGTTAGAGGATCTACCTACTGTT 458
QY 361 GAGGCTCCTGGAGATCCTCAAGAACCCAGAAATAATGCCACAGGGACAAAGAGGGAT 420
Db 459 GAGGCTCCTGGAGATCCTCAAGAACCCAGAAATAATGCCACAGGGACAAAGAGGGAT 518
QY 421 GACCAGAGTCATTGGCGCTATGGAGGCGACCCCGCTGGCCCGGGTGTCCCCAGCCTGC 480
Db 519 GACCAGAGTCATTGGCGCTATGGAGGCGACCCCGCTGGCCCGGGTGTCCCCAGCCTGC 578
QY 481 GCGGGCCGCTTCAGTCCCGGTGGATATCCGCCCCAGCTCGCCGCTTCTGCCCGGCC 540
Db 579 GCGGGCCGCTTCAGTCCCGGTGGATATCCGCCCCAGCTCGCCGCTTCTGCCCGGCC 638
QY 541 CTGCGCCCCCTGGAACCTCCTGGGCTTCAGCTCCCGCGCTCCAGAACTGCGCCTGCGC 600
Db 639 CTGCGCCCCCTGGAACCTCCTGGGCTTCAGCTCCCGCGCTCCAGAACTGCGCCTGCGC 698
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QY 780 CACCGCCTTTCAGAGATTGACGAGGCTTGGGGCGCCCGGAGGCGCTGGCCGTGTTGGC 839
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Db 939 CGCCTTTCAGAGAGGGG-CCGGRAGAAACAGTGCCTATGAGCAGTTGCTGTCTCGCTT 997
QY 900 GGAAGAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCCAGGACTGGACATATCTGCACT 959
Db 998 GGAAGAAATCGCTGAGGAA-GCTCAGAGACTYAGGKYCCAGGACTGGACAAATCTGCACT 1056
QY 960 CCTGCCCTCTGACTTCAGCCGCTACTTCCAATATGAGGGGTCTCTGACTACACCGCCCTG 1019
Db 1057 C--TGSCCTCTGACTTCAG-CGCTAMTTCCAWAGAGGGTCTCT--KATWMACCGCCCTK 1110
QY 1020 TGCCCCAGG 1027
Db 1111 TGCCAGGG 1118

BX423970
LOCUS BX423970 Homo sapiens NEUROBLASTOMA Homo sapiens linear EST 15-MAY-2003
DEFINITION CS0DA003YB12 5-PRIME, mRNA sequence.
ACCESSION BX423970
VERSION BX423970.1 GI:30766328
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 1013)
JOURNAL Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
COMMENT Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5300.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS1DA001ZF09QP1&cluster=5300.f. Contact :
Peng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS1DA001ZF09QP1.
Location/Qualifiers
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/tissue_type="NEUROBLASTOMA"
/clone_lib="Homo sapiens NEUROBLASTOMA"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dt) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
ORIGIN
Query Match 60.1%; Score 915; DB 13; Length 1013;
Best Local Similarity 94.6%; Pred.No. 3.2e-193;
Matches 906; Conservative 33; Mismatches 19; Indels 0; Gaps 0;
QY 2 CAGTCAGCCGATGGCTCCCTGTGCCCCAGCCCTGGCTCCCTCTGTTGATCCCGGCC 61
Db 56 CCGGGATCCGATGGCTCCCTGTGCCCCAGCCCTGGCTCCCTCTGTTGAWCCCGGCC 115
QY 62 CTGCTCCAGGCCTCACTGTGCAACTGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 121
Db 116 CTGCTCCAGGCCTCACTGTGCAACTGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 175
QY 122 CCCAGAGTTGCCCGGATGCAGGAGGATCCCCCTTGGGAGGAGCTCTTCTGGGGAAG 181
Db 176 CCCAGAGTTGCCCGGATGCAGGAGGATCCCCCTTGGGAGGAGCTCTTCTGGGGAAG 235
QY 182 ATGACCCACTGGCGGAGGAGGATCTGCCAGTGAAGAGGATTCAACCAGAGAGGAGATC 241
Db 236 ATGACCCACTGGCGGAGGAGGATCTGCCAGTGAAGAGGATTCAACCAGAGAGGAGATC 295
QY 242 CACCCGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTG 301
Db 296 CACCCGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCWACCTG 355
QY 302 AAGTTAAGCCTAAATCAGAAGAACAGAGGGCTCCCTGAAGTTAGAGGATCTACCTACTGTTG 361
Db 356 AAGTTAAGCCTAAATCAGAAGAACAGAGGGCTCCCTGAAGTTAGAGGATCTACCTACTGTNG 415
QY 362 AGGCTCCTGGAGATCCTCAAGAACCCCAAGATAATGCCACAGGGACAAAGAGGGGATG 421
Db 416 AGGCTCCTGGAGAACCTCAAGAACMCCAGAATAAAGGCCACAGGGACAAAGAGGGGATG 475


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QY 901 GAAGAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCAGGACTGGACATATCTGCACTC 960
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Db 992 GAA-RAATCGCTGAGGAA-GCTCAGAGACTCAGGKCCAGGACTGGACAWAT-TGCACTC 1048

QY 961 CTGCC 965
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Db 1049 CTGCC 1053

RESULT 5
AL554665/c
LOCUS
DEFINITION
AL554665 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0DI085YF18 3-PRIME, mRNA sequence.
ACCESSION
AL554665
VERSION
AL554665.2 GI:31276475
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1201)
AUTHORS
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE
Full-length cDNA libraries and normalization
JOURNAL
Unpublished (2001)
COMMENT
On Feb 15, 2001 this sequence version replaced gi:12895665.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5300.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DI085DC09NP1&cluster=5300.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DI085DC09NP1.

FEATURES
            Location/Qualifiers
source          1..1201
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="CS0DI085YF18"
                /tissue_type="PLACENTA COT 25-NORMALIZED"
                /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                /note="1st strand cDNA was primed with a NotI-oligo(dT)
                primer. Five prime end enriched, double-strand cDNA was
                digested with Not I and cloned into the Not I and EcoR V
                sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Query Match          56.8%; Score 865.2; DB 9; Length 1201;
Best Local Similarity 92.0%; Pred. No. 4.6e-182;
Matches 1027; Conservative 23; Mismatches 47; Indels 19; Gaps 13;

QY 407 ACAAGAAGGGGATGACACAGAGTCAATTGGCGCTATGGAGGCGACCGCCCTGGCCCCGGG 466
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Db 1108 AGAAAAAARGGGATACCAAAATTAWTTGGCTATGAAGGC--ACCGCCCTTGSCCCSGG 1051

QY 467 TGTCCCCAGCCTGCGCGGCGCGCTTCCAGTCCCGGTGGATATCCGCCCCCGAGCTCGCGG 526
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1050 TGTCCCCAGCCTGCGC-GGCCGCTHCMAGTCCCGGT-GATATCCGCCCCCGG-TYGCCG 994

QY 527 CCTTCTGCCCCGCTGCGCCCCCTGGAACTCTCGGGCTTCCAGTCCCGCCGCTCCCGAG 586
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 993 CCTTCTGCCCCG-CCYGGGCCCCYTGGA--CTCCTGGSTTCVGTCCSCCGCTCCCGAG 937

QY 587 AACTGCGCCTGCGCAACAATGGCCACAGTGTGCAACTGACCCCTGCTCTGGGCTAGAGA 646
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Db 936 RACTGCG-CTGCGCAACAATGGCCACAGTGTGCAACTGACCCCTGCTCTGGGCTAGAGA 878
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QY 647 TGGCTCTGGGTCCCGGGCGGGAGTACCGGGCTCTGCAGCTGCATCTGCACCTGGGGGCTG 706
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Db 877 TGGCTCTGGGTCCCGGGCGGGAGTACCGGGCTCTGCAGCTGCATCTGMACTGGGGGCTG 818

QY 707 CAGGTCTCGGGGCTCGGAGCACACTGTGGAAGGCCACCGTTTCCCTGCCGAGATCCACG 766
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Db 817 CAGGTCTCGGGGCTCGGRGCACACTGTGGAAGGCCACCGTTTCCCTGCCGAGATCCACG 758

QY 767 TGGTTCACCTCAGCACCGCCCTTTGCCAGAGTTGACGAGGCCCTTGGGGCGCCCGGAGGCC 826
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Db 757 TGGTTCACCTCAGCACCGCCCTTTGCCAGAGTTGACGAGGCCCTTGGGGCGCCCGGAGGCC 698

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Db 637 GGCTSTCTCGCTTGGAAAGMAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCCAGCAGT 578

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Db 457 CTGAGTGTAAAGCAGCTCCACACCCCTCTCTGACACCCCTGTGGGGACCTGGTAACTCTCGG 398

QY 1123 CTACAGCTGAACCTCCGAGCGACGAGCCCTTTGAAATGGGCGAGTGAATTCCTGCCTG 1182
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Db 397 CTACAGCTGAACCTCCGAGCGACGAGCCCTTTGAAATGGGCGAGTGAATTCCTGCCTC 338

QY 1183 CCTGTGGAGTGGACAGCAGTCTCGGGCTGTCTGAGCCAGTCCAGCTGAATTCCTGCCTG 1242
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Db 337 CCTGTGGAGTGGACAGCAGTCTCGGGCTGTCTGAGCCAGTCCAGCTGAATTCCTGCCTG 278

QY 1243 GCTGTGTGACATCTAGCCCTGTGTTTGGCCCTCCTTTTGTGCTCACCAGCGTCGCG 1302
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QY 1363 CCAGCAGAGGTAGCCGAGACTGGAGC---CTAGAGGCTGGATCTTGGAGAAATGTGAGAAG 1419
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QY 1420 --CCAGCCAGAGGCATCTGAGGGGGAGCCGGTAACTGTCTCTGCTCATTATG-CCA 1476
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Db 97 ACACAGCCAGAGGCATCTGAGGGGGAGCCGGTNACTGTCTCTGCTCATTATGNCCA 38

QY 1477 CTTCCCTTTAACTGCCAAGAAATTTTAAATAAA 1512
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Db 37 CTTCCCTTTTNACTGCCAANNMVMVTTTAAWWATAA 2
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RESULT 6
BX401186
LOCUS
DEFINITION
BX401186 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens
cDNA clone CS0DK009YP10 5-PRIME, mRNA sequence.
ACCESSION
BX401186
VERSION
BX401186.1 GI:30626393
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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REFERENCE 1 (bases 1 to 1201)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5300.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DK009DH05QP1&cluster=5300.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVtroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DK009DH05QP1.

FEATURES
source
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DK009YP10"
/cell_type="HELA CELLS COT 25-NORMALIZED"
/cell_line="HELA"
/clone_lib="Homo sapiens HELA CELLS COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Query Match 54.7%; Score 832; DB 13; Length 1201;
Best Local Similarity 97.4%; Pred. No. 1.2e-174;
Matches 896; Conservative 3; Mismatches 13; Indels 8; Gaps 5;

QY 1 ACAGTCAGCCGATGGCTCCCTGTGCCCCAGCCCTGGCTCCCTCTGTGATCCCGGCC 60
Db 51 ACAGTCAGCCGATGS-TCCCTGTGCCCCAGCCCTGGCTCCCTCTGTGATCCCGGCC 109
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QY 121 CCCAGAGGTTGCCCGGATGAGGAGGATTCCCCCTGGGAGGAGGCTTCTTGGGGAA 180
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QY 181 GATGACCCACTGGCGGAGGAGGATCTGCCAGTGAAGAGGATTACCCAGAGGAGGAT 240
Db 230 GATGACCCACTGGCGGAGGAGGATCTGCCAGTGAAGAGGATTACCCAGAGGAGGAT 289
QY 241 CCACCCGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCT 300
Db 290 CCACCCGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCT 349
QY 301 GAAGTTAAGCCTAAATCAGAAGAAGAGGGCTCCCTGAAGTTAGAGGATCTACTGTT 360
Db 350 GAAGTTAAGCCTAAATCAGAAGAAGAGGGCTCCCTGAAGTTAGAGGATCTACTGTT 409
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Db 410 GAGGCTCTGGAGATCCTCAAGAACCCCCAGATAATGCCACAGGGACAAAGAAGGGAT 469
QY 421 GACCAGATCATTTGGCGCTATGAGGCGACCCGCCCTGGCCCCGGGTGTCCCGAGCCTGC 480
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QY 541 CTGCGCCCCCTGGAATCTCTGGGCTTCCAGCTCCCGCGCTCCCGAGAACTGCGCTGCGC 600

Db 590 CTGCGCCCCCTGGAACCTCCTGGGCTTCCAGCTCCCGCGCTCCAGAACTGCGCCTGCGC 649
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Db 830 ACCGCCTTTGCCAGAGTTGACGAGGCCCTTGGGCGGCCCGGAGG-CTGGCCGTGTTGG-C 887
QY 841 GCCTTTCTGGAGGAGGCCCGGAGAAACACAGTGCCTATGAGCAGTTCGTGCTCGCTTG 900
Db 888 GCCTTTCTGGAGGAGG--CCCGGAAGAAACAGTGCCTATGAGCAGT---TGYGTCTCGCT 942
QY 901 GAAGAAATCGCTGAGGAAG 920
Db 943 GGWAGAATCGCTGAGGAAG 962

RESULT 7
BX423969/c
LOCUS BX423969 Homo sapiens NEUROBLASTOMA Homo sapiens cDNA clone
DEFINITION CS0DA003YB12 3-PRIME, mRNA sequence.
ACCESSION BX423969
VERSION BX423969.1 GI:30766327
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1007)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5300.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS1DA001ZF09NP1&cluster=5300.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVtroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS1DA001ZF09NP1.

FEATURES
source
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DA003YB12"
/tissue_type="NEUROBLASTOMA"
/clone_lib="Homo sapiens NEUROBLASTOMA"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."

ORIGIN
Query Match 53.5%; Score 813.6; DB 13; Length 1007;
Best Local Similarity 89.7%; Pred. No. 1.4e-170;
Matches 852; Conservative 24; Mismatches 71; Indels 3; Gaps 2;

[illegible]

KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1031)
Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 16, 2001 this sequence version replaced gi:12941176.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5300.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DK007BF05NP1&cluster=5300.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DK007BF05NP1.
Location/Qualifiers
1. 1031
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DK007YK10"
/cell_type="HELA CELLS COT 25-NORMALIZED"
/cell_line="HELA"
/clone_lib="Homo sapiens HELA CELLS COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

FEATURES
source

ORIGIN

	Query Match	52.4%;	Score 796.8;	DB 9;	Length 1031;	
	Best Local Similarity	86.0%;	Pred. No. 7.9e-167;			
	Matches 852;	Conservative 50;	Mismatches 84;	Indels	Gaps	4
QY	521	TGCGCGCTTCTGCCCCGGCCTGCGCCCCCTTGAACTCCTGGGCTTCAGACTCCGGCCGC	580			
DB	989	TCCSCCCNGCTCCCSCTTYKGC CGCCCTCSCCCCKGAAYTCTGGTSCCKTCCCGC	930			
QY	581	TCCCAGAACTGCGCTGCGCAACAATGGCCACAGTGTGCAACTGACCCTGCCTCCTGGGC	640			
DB	929	CYYCCGMGVACTCTCCTCKMACAAKGGCCACA-KGTGCMAYTMCCYTSCYGYKGGGC	871			
QY	641	TAGAGATGGCTCTGGGTCCGGGCGGGAGTACCGSGTCTGCAGCTGCATCT-CGACTGG	699			
DB	870	KAGAGATGGCTCTGGGTCCGGGCGGGAGTACCGSGTCTGCAGYGTCTWTSTKGCAKGG	811			
QY	700	GGGGTGCAGGTCGTCCGGGCTCGGAGCACACTGTGGAAGGCCACCCTTTCCCTGCCCAG	759			
DB	810	GGNGCTCAGGKCGTCKGGSTCGGAGCACATGGGGGAAGGCCACCCTGTCGCCGCCGAG	751			
QY	760	ATCACGTGGTTCACTCAGCACCGCCTTTGCCACAGTTGACGAGGCCCTTGGGGCGCCCCG	819			
DB	750	ATCASGGGGTKAACCTCAGCACCGCCTTTGCCACAGTTGACGAGGCC-TKGGCGCCCCG	692			
QY	820	GGAGCCTGGCCGTGTTGGCCGCCCTTTCTGGAGGAGGGCCCGGAAGAAAACAGTGCCCTAT	879			
DB	691	GGAGCCTGGCCGTGTTGGCCGCCCTKTCTGGAGGAGGGCCCGGAAGAAAACAGGGCCTAT	632			
QY	880	GAGCAGTTGCTGTCTCGTTGGAGAAAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCCCA	939			
DB	631	GAGCAGTTGCTGTCTCGTTGGAGAAAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCCCA	572			
QY	940	GGACTGGACATACTGCACTCTGCCCTCTGACTTTCAGCCCGCTACTTCCAATATGAGGGG	999			
DB	571	GNACTGGACATATCTGCACTCTGCCCTCTRACTTTCANCCACTACTHCCAATGAGGGG	512			

/clone="IMAGE:4583869"
/tissue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC_15"
/note="Organ: colon; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)"

ORIGIN

Query Match 48.1%; Score 731.4; DB 12; Length 874;
Best Local Similarity 94.8%; Pred. No. 2.9e-152;
Matches 822; Conservative 0; Mismatches 36; Indels 9; Gaps 6;

QY 207 GCCAGTGAAGAGGATTCCACCAGAGAGGAGGATCCACCCGGAGAGGAGGATCTACCTGG 266
Db 1 GCCCAGTGAAGAGGATTCCACCAGAGAGGAGGATCCACCCGGAGAGGAGGATCTACCTGG 60

QY 267 AGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGAAGTTAAGCCTAAATCAGAAGAAGA 326
Db 61 AGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGAAGTTAAGCCTAAATCAGAAGAAGA 120

QY 327 GGGCTCCCTGAAGTTAGAGGATCTACCTACTGTTAGGCTCCTGGAGATCCTCAAGAACC 386
Db 121 GGGCTCCCTGAAGTTAGAGGATCTACCTACTGTTAGGCTCCTGGAGATCCTCAAGAACC 180

QY 387 CCAGATAATGCCCCACAGGGACAAGAAGGGGATGACCAGAGTCATTGGCGGTATGGAGG 446
Db 181 CCAGATAATGCCCCACAGGGACAAGAAGGGGATGACCAGAGTCATTGGCGGTATGGAGG 240

QY 447 CGACCCGCCCTGGCCCCGGGTGTCCCCAGCCTGCGGGGGCGCTTCCAGTCCCGGTGGA 506
Db 241 CGACCCGCCCTGGCCCCGGGTGTCCCCAGCCTGCGGGGGCGCTTCCAGTCCCGGTGGA 300

QY 507 TATCCGGCCCCAGCTCGCCGCTTCTGCCCCGCTTCCGCCCCCTGGAACCTCTGGGCTT 566
Db 301 TATCCGGCCCCAGCTCGCCGCTTCTGCCCCGCTTCCGCCCCCTGGAACCTCTGGGCTT 360

QY 567 CCAGTCCCGCGCTCCAGAACTCGCCCTGCGCAACAATGGCCACAGTGTGCAACTGAC 626
Db 361 CCAGTCCCGCGCTCCAGAACTCGCCCTGCGCAACAATGGCCACAGTGTGCAACTGAC 420

QY 627 CCTGCTCCTGGGCTAGAGATGCTTGGTCCCGGGGGGAGTACCGGGCTCTGCAGCT 686
Db 421 CCTGCTCCTGGGCTAGAGATGCTTGGTCCCGGGGGGAGTACCGGGCTCTGCAGCT 480

QY 687 GCATCTGCACTGGGGGCTGCAGTCTGCTCGGGCTCGGAGCACACTGTGGAAAGGCCACCG 746
Db 481 GCATCTGCACTGGGGGCTGCAGTCTGCTCGGGCTCGGAGCACACTGTGGAAAGGCCACCG 540

QY 747 TTTCCCTGCGGAGATCCACGTGTTACCTCAGCACCGCCTTTCGCCAGAGTTGACGAGGC 806
Db 541 TTTCCCTGCGGAGATCCACGTGTTACCTCAGCACCGCCTTTCGCCAGAGTTGACGAGGC 600

QY 807 CTTGGGGCGCCGGAGGCTGGCGGTGTTGGCGGCTTCTTGAGGAGGGCCGGAAGA 866
Db 601 CTTGGGGCGCCGGAGGCTGGCGGTGTTGGCGGCTTCTTGAGGAGGGG-CCGGAAGA 659

QY 867 AAACAGTGCTATGAGCAGTTGCTGCTCGCTTGGGAAGAAATCGCTGAGGAAGGCTCAGA 926
Db 660 CAACAGTGCTATGAGCAGTTGCTGCTCGCTTGGGAAGAAATCGCTGAGGAAGGCTCAGA 719

QY 927 GACTC--AGTCCCAGGACTGGAC---ATATCTGCACCTCTGCCCTCTGACTTCAGCCGC 981
Db 720 GAATCCAGGGCCCAAGGACTGGACATTAATCTTGAATCTTGACCTTCTGACTTCAAGCGG 779

QY 982 TAC-TTCCAATATAGGGGTCT-CTGACTACACCGCCCTGTGCCCCAGGGTGTCACTCTGGA 1039
Db 780 TACTTTCCAATATAGGGGCTTCCGGAATACACCGGCCCTGTGTACACAGGGTGTCA-CCGGA 838

QY 1040 CTGTGTTTAAACCAGACAGCTGATGCTGA 1066
Db 839 GTGTGTTTACCAGACATGATGCTTA 865

RESULT 12
CA425935/c
LOCUS
DEFINITION
UI-H-FEI-beg-j-10-0-UI.s1 NCI_CGAP_FEI Homo sapiens cDNA clone
UI-H-FEI-beg-j-10-0-UI 3', mRNA sequence.
ACCESSION
CA425935
VERSION
CA425935.1 GI:24788661
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 689)
AUTHORS
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL
Unpublished (1997)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: James Martin
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA
sequence: 1-42, >AT rich#Low_complexity (matched compliment)
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FEI-beg-j-10-0-UI"
/tissue_type="Cell lines"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP FEI"
/note="Organ: Chondrosarcoma; Vector: pT7T3-Pac
(Pharmacia) with a modified polylinker; Site 1: EcoR I;
Site 2: Not I; NCI_CGAP_FEI is a normalized cDNA library
derived from a pool of mRNA obtained from 3 cell lines
from grade II chondrosarcoma tissues. The library was
constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pT7T3-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
CGCTACGGAC. The cell lines were provided by Dr James
Martin from the University of Iowa.
TAG_TISSUE=Human grade 2 chondrosarcoma cell line pool
TAG_LIB=UI-H-FEI
TAG_SEQ=CGCTACGGAC"

ORIGIN

Query Match 44.0%; Score 669.8; DB 14; Length 689;
Best Local Similarity 99.6%; Pred. No. 1.4e-138;
Matches 671; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 849 GGAGGAGGGCCCGGAAGAAACAGTGCCTATGAGCAGTTGCTCTCGCTTGGAGAAAT 908
Db 689 GGAGGAGGGCCCGGAAGAAACAGTGCCTATGAGCAGTTGCTCTCGCTTGGAGAAAT 630

QY	909	CGCTGAGGAAGGCTCAGAGACTCAGGTCCCAGGACTGGACATATCTGCACTCCTGCCCCTC	968
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QY	969	TGACTTCAGCCGCTACTTCCAAATATGAGGGGTCTCTGACTACACGCCCTGTGCCAGGG	1028
DB	569	TGACTTCAGCCGCTACTTCCGATATGAGGGGTCTCTGACTACACGCCCTGTGCCAGGG	510
QY	1029	TGTCATCTGGACTGTGTTAAACCAAGACAGTGATGCTGAGTGTAAAGCAGCTCCACACCTT	1088
DB	509	TGTCATCTGGACTGTGTTAAACCAAGACAGTGATGCTGAGTGTAAAGCAGCTCCACACCTT	450
QY	1089	CTCTGACACCCCTGTGGGACCTGGTGACTCTCGGCTACAGCTGAACTTCCGAGCGACGCA	1148
DB	449	CTCTGACACCCCTGTGGGACCTGGTGACTCTCGGCTACAGCTGAACTTCCGAGCGACGCA	390
QY	1149	GCCTTTGAATGGCGAGTGATTTGAGGCCCTCCTTCCCTGCTGGAGTGGACAGCATCTCTCG	1208
DB	389	GCCTTTGAATGGCGAGTGATTTGAGGCCCTCCTTCCCTGCTGGAGTGGACAGCATCTCTCG	330
QY	1209	GGCTGCTGAGCCAGTCCAGCTGAATTCCTGCCTGGCTGGTGACATCCTAGCCCTGGT	1268
DB	329	GGCTGCTGAGCCAGTCCAGCTGAATTCCTGCCTGGCTGGTGACATCCTAGCCCTGGT	270
QY	1269	TTTTGGCCCTCCTTTTGTGCTGTACCAGCGTCGGCTTCTTGTGCAGATGAGAAGGCAGCA	1328
DB	269	TTTTGGCCCTCCTTTTGTGCTGTACCAGCGTCGGCTTCTTGTGCAGATGAGAAGGCAGCA	210
QY	1329	CAGAAGGGGAACCAAGGGGGTGTGAGCTACGCCAGCAGAGGTAGCCGAGACTGGAGC	1388
DB	209	CAGAAGGGGAACCAAGGGGGTGTGAGCTACGCCAGCAGAGGTAGCCGAGACTGGAGC	150
QY	1389	CTAGAGGCTGGATCTTTGGAGAAATGTGAGAAAGCCAGCCAGAGGCATCTGAGGGGAGCCGG	1448
DB	149	CTAGAGGCTGGATCTTTGGAGAAATGTGAGAAAGCCAGCCAGAGGCATCTGAGGGGAGCCGG	90
QY	1449	TAACTGCTCCTGCTCATTTATGCCACTTCCCTTTTAACTGCCAAGAAATTTTTTAAAA	1508
DB	89	TAACTGCTCCTGCTCATTTATGCCACTTCCCTTTTAACTGCCAAGAAATTTTTTACAA	30
QY	1509	TAAATATTTTATAAT	1522
DB	29	TAAATATTTTATAAT	16

RESULT 13
AI831707/c
LOCUS
DEFINITION
wJ40h01.x1 NCI CGAP Lu19 Homo sapiens CDNA clone IMAGE:2405329 3',
similar to TR:Q16790 Q16790 CARBONIC ANHYDRASE ;, mRNA sequence.
AI831707
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
EST.
AI831707.1 GI:5452464
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 682)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

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High quality sequence stop: 424.
FEATURES
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            /lab_host="DH10B (phage-resistant)"
            /clone_lib="NCI_CGAP_Lu19"
            /note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a
            modified polylinker; 1st strand cDNA was prepared from
            pooled lung tumor tissue, and was then primed with a Not I
            - oligo(dT) primer. Double-stranded cDNA was ligated to
            Eco RI adaptors (Pharmacia), digested with Not I and
            cloned into the Not I and Eco RI sites of the modified
            pT7T3 vector. Library went throughb one round of
            normalization. Library constructed by Bento Soares and M.
            Fatima Bonaldo."

```

Query Match		43.7%;	Score 665.8;	DB 9;	Length 682;
Best Local Similarity		98.8%;	Pred. No. 1.1e-137;		
Matches	670;	Conservative	0;	Mismatches	8;
				Indels	0;
				Gaps	0;
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QY	905	AAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCCAGGACTGGACATATCTGCACCTCCTGC	964		
DB	618	ACATCGCTGAGGAAGGCTCAGAGACTCAGGTCCCAGGACTGGACATATCTGCACCTCCTGC	559		
QY	965	CCTCTGACTTCAGCCGCTACTTCCAAATATAGGGGTCTCTGACTACACGCCCTGTGCCC	1024		
DB	558	CTTCTGACTTCAGCCGCTACTTCCAAATATAGGGGTCTCTGACTACACGCCCTGTGCCC	499		
QY	1025	AGGGTGTCACTGGACTGTGTTTAAACCAGACAGTGAATGCTGAGTGTAAAGCAGCTCCACA	1084		
DB	498	AGGGTGTCACTGGACTGTGTTTAAACCAGACAGTGAATGCTGAGTGTAAAGCAGCTCCACA	439		
QY	1085	CCCTCTCTGACACCCCTGTGGGGACCTGGTGACTCTCGGCTACAGCTGAACCTCCGAGCGA	1144		
DB	438	CCCTCTCTGACACCCCTGTGGGGACCTGGTGACTCTCGGCTACAGCTGAACCTCCGAGCGA	379		
QY	1145	CGCAGCCTTTGAATGGCGAGTGATTGAGGCCCTCTTCCCTGCTGGAGTGGACAGCAGTC	1204		
DB	378	CGCAGCCTTTGAATGGCGAGTGATTGAGGCCCTCTTCCCTGCTGGAGTGGACAGCAGTC	319		
QY	1205	CTCGGGCTGCTAGCCAGTCCAGCTGAATCTCTGCCCTGGCTGCTGGTGACATCCTAGCCC	1264		
DB	318	CTCGGGCTGCTAGCCAGTCCAGCTGAATCTCTGCCCTGGCTGCTGGTGACATCCTAGCCC	259		
QY	1265	TGGTTTTTGGCTCTTTTGTGCTGTACCAAGCGTGCCTTCTTGTGCAGATGAGAAGGC	1324		
DB	258	TGGTTTTTGGCTCTCTTTTGTGCTGTACCAAGCGTGCCTTCTTGTGCAGATGAGAAGGC	199		
QY	1325	AGCACAGAGGGGAACCAAGGGGTGTGAGCTACCGCCCGAGCAGAGGTAGCCGAGACTG	1384		
DB	198	AGCACAGAGGGGAACCAAGGGGTGTGAGTACCGCCCGAGCAGAGGTAGCCGAGACTG	139		
QY	1385	GAGCCTAGAGGCTGGATCTTGGAGAAATGTGAGAAGCCAGCCAGGCGATCTGAGGGGGAG	1444		
DB	138	GAGCCTAGAGGCTGGATCTTGGAGAAATGTGAGAAGCCAGCCAGGCGATCTGAGGGGGAG	79		
QY	1445	CCGGTAACTGTCCTGTCTGCTCATTTATGCCACTTCTTTTAACTGCCAAGAAATTTTTT	1504		
DB	78	CCGGTAACTGTCCTGTCTGCTCATTTATGCCACTTCTTTTAACTGCCAAGAAATTTTTT	19		

GenCore version 5.1.6
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OMnucleic - nucleic search, using sw model

Run on: May 11, 2004, 12:31:03 ; Search time 127 Seconds
(without alignments)
6650.671 Million cell updates/sec

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Perfect score: 1522
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: /cgn2_6/ptodata/2/ina/6B COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1522	100.0	1522	2	US-08-481-658B-1 Sequence 1, Appli
2	1522	100.0	1522	2	US-08-477-504A-1 Sequence 1, Appli
3	1522	100.0	1522	2	US-08-486-756A-1 Sequence 1, Appli
4	1522	100.0	1522	2	US-08-485-862B-1 Sequence 1, Appli
5	1522	100.0	1522	3	US-08-787-739-1 Sequence 1, Appli
6	1522	100.0	1522	3	US-08-487-077A-1 Sequence 1, Appli
7	1522	100.0	1522	3	US-08-485-863A-1 Sequence 1, Appli
8	1522	100.0	1522	3	US-08-485-049D-1 Sequence 1, Appli
9	1522	100.0	1522	3	US-09-178-115-1 Sequence 1, Appli
10	1522	100.0	1522	3	US-09-177-776-1 Sequence 1, Appli
11	1399	91.9	1399	3	US-08-335-469-1 Sequence 1, Appli
12	1302.8	85.6	1397	1	US-07-964-589-1 Sequence 1, Appli
13	1302.8	85.6	1397	5	PCT-US93-02024-1 Sequence 1, Appli
14	414.4	27.2	10898	2	US-08-481-658B-5 Sequence 5, Appli
15	414.4	27.2	10898	2	US-08-477-504A-5 Sequence 5, Appli
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19	414.4	27.2	10898	3	US-08-487-077A-5 Sequence 5, Appli
20	414.4	27.2	10898	3	US-08-485-863A-5 Sequence 5, Appli
21	414.4	27.2	10898	3	US-08-485-049D-5 Sequence 5, Appli
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23	414.4	27.2	10898	3	US-09-177-776-5 Sequence 5, Appli
24	413.4	27.2	415	2	US-08-481-658B-28 Sequence 28, Appli
25	413.4	27.2	415	2	US-08-477-504A-28 Sequence 28, Appli
26	413.4	27.2	415	2	US-08-486-756A-28 Sequence 28, Appli
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28	413.4	27.2	415	3	US-08-487-077A-28 Sequence 28, Appli
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31	413.4	27.2	445	3	US-08-787-739-28 Sequence 28, Appli
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35	233.4	15.3	470	2	US-08-477-504A-55 Sequence 55, Appli
36	233.4	15.3	470	2	US-08-486-756A-55 Sequence 55, Appli
37	233.4	15.3	470	2	US-08-485-862B-55 Sequence 55, Appli
38	233.4	15.3	470	3	US-08-787-739-55 Sequence 55, Appli
39	233.4	15.3	470	3	US-08-487-077A-55 Sequence 55, Appli
40	233.4	15.3	470	3	US-08-485-863A-55 Sequence 55, Appli
41	233.4	15.3	470	3	US-08-485-049D-55 Sequence 55, Appli
42	233.4	15.3	470	3	US-09-178-115-55 Sequence 55, Appli
43	233.4	15.3	470	3	US-09-177-776-55 Sequence 55, Appli
44	191	12.5	191	2	US-08-481-658B-38 Sequence 38, Appli
45	191	12.5	191	2	US-08-477-504A-38 Sequence 38, Appli

ALIGNMENTS

RESULT 1
US-08-481-658B-1
; Sequence 1, Application US/08481658B
; Patent No. 5955075
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: 6 Mariposa Court
; CITY: Tiburon
; STATE: California
; COUNTRY: USA
; ZIP: 94920
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/481,658B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/260,190
; FILING DATE: 15-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863
; REFERENCE/DOCKET NUMBER: D-0021.3E
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-435-2034
; TELEFAX: 415-435-0727
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1522 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-481-658B-1

Query Match 100.0%; Score 1522; DB 2; Length 1522;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ACAGTCAGCCGCATGGCTCCCTGTGCCCCAGCCCCCTGGCTCCCTCTGTGTGATCCCGGCC	60
Db	1	ACAGTCAGCCGCATGGCTCCCTGTGCCCCAGCCCCCTGGCTCCCTCTGTGTGATCCCGGCC	60
QY	61	CCTGCTCCAGGCCTCACTGTGCAACTGCTGCTGTCACTGCTGCTTCTGTATGCCTGTCCAT	120
Db	61	CCTGCTCCAGGCCTCACTGTGCAACTGCTGCTGTCACTGCTGCTTCTGTATGCCTGTCCAT	120
QY	121	CCCCAGAGTTGCCCGGATGCAAGGAGTATCCCCCTTTGGGAGGAGGCTCTTCTGGGAA	180
Db	121	CCCCAGAGTTGCCCGGATGCAAGGAGTATCCCCCTTTGGGAGGAGGCTCTTCTGGGAA	180
QY	181	GATGACCCACTGGGCGAGGAGGATCTGCCCCAGTGAAGAGGATTACCCAGAGAGGAGGAT	240
Db	181	GATGACCCACTGGGCGAGGAGGATCTGCCCCAGTGAAGAGGATTACCCAGAGAGGAGGAT	240
QY	241	CCACCCGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCT	300
Db	241	CCACCCGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCT	300
QY	301	GAAGTTAAGCCTAAATCAGAAGAAAGAGGGCTCCCTGAAGTTAGAGGATCTACCTACTGTT	360
Db	301	GAAGTTAAGCCTAAATCAGAAGAAAGAGGGCTCCCTGAAGTTAGAGGATCTACCTACTGTT	360
QY	361	GAGGCTCCTGGAGATCCTCAAGAAACCCAGAAATAATGCCACAGGGACAAAGAAGGGGAT	420
Db	361	GAGGCTCCTGGAGATCCTCAAGAAACCCAGAAATAATGCCACAGGGACAAAGAAGGGGAT	420
QY	421	GACCAGAGTCATTGGCGCTATGGAGGGGACCCGCCCTGGCCCCCGGGTGTCCCCAGCCTGC	480
Db	421	GACCAGAGTCATTGGCGCTATGGAGGGGACCCGCCCTGGCCCCCGGGTGTCCCCAGCCTGC	480
QY	481	GCGGGCCGCTTCCAGTCCCGGTGGATATCCGCCCCAGTCCCGCCTTCTGCCCGGCC	540
Db	481	GCGGGCCGCTTCCAGTCCCGGTGGATATCCGCCCCAGTCCCGCCTTCTGCCCGGCC	540
QY	541	CTGCGCCCCCTGGAACTCCTGGCTTCCAGCTCCCGCGCTCCAGAACTGCGCCTGCGC	600
Db	541	CTGCGCCCCCTGGAACTCCTGGCTTCCAGCTCCCGCGCTCCAGAACTGCGCCTGCGC	600
QY	601	AACAATGGCCACAGTGTGCAACTGACCCCTGCCTCCTGGGCTAGAGATGGCTCTGGGTCCC	660
Db	601	AACAATGGCCACAGTGTGCAACTGACCCCTGCCTCCTGGGCTAGAGATGGCTCTGGGTCCC	660
QY	661	GGGCGGGAGTACCGGGTCTGCAGCTGCATCTGCACTGGGGGGCTGCAGGTGCTCCGGGC	720
Db	661	GGGCGGGAGTACCGGGTCTGCAGCTGCATCTGCACTGGGGGGCTGCAGGTGCTCCGGGC	720
QY	721	TCGGAGCACACTGTGGAAGGCCACCGTTTCCCTGCCGAGATCCACGTGTTTCACTCAGC	780
Db	721	TCGGAGCACACTGTGGAAGGCCACCGTTTCCCTGCCGAGATCCACGTGTTTCACTCAGC	780
QY	781	ACCGCCTTTGCCAGAGTTGACGAGGCCCTTGGGGCGCCCGGGAGGCCCTGGCCGTGTGGCC	840
Db	781	ACCGCCTTTGCCAGAGTTGACGAGGCCCTTGGGGCGCCCGGGAGGCCCTGGCCGTGTGGCC	840
QY	841	GCCTTTCTGGAGGGGCCCGGAAGAAACAGTGCCTATGAGCAGTTGCTGCTCGCTTG	900
Db	841	GCCTTTCTGGAGGGGCCCGGAAGAAACAGTGCCTATGAGCAGTTGCTGCTCGCTTG	900
QY	901	GAAGAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCAGGACTGGACATATCTGCACTC	960
Db	901	GAAGAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCAGGACTGGACATATCTGCACTC	960
QY	961	CTGCCCTCTGACTTACGCCGCTACTTCCAATATGAGGGGTCTCTGACTACACCCGCTGT	1020
Db	961	CTGCCCTCTGACTTACGCCGCTACTTCCAATATGAGGGGTCTCTGACTACACCCGCTGT	1020
QY	1021	GCCCAGGGTGTCACTGGACTGTGTTTAAACCAGACAGTGTGCTGAGTGTAAAGCAGCTC	1080
Db	1021	GCCCAGGGTGTCACTGGACTGTGTTTAAACCAGACAGTGTGCTGAGTGTAAAGCAGCTC	1080

RESULT 2

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US-08-477-504A-1
; Sequence 1, Application US/08477504A
; Patent No. 5972353
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: 6 Mariposa Court
; CITY: Tiburon
; STATE: California
; COUNTRY: USA
; ZIP: 94920
; COMPUTER READABLE FORM:
; MEDIA TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,504A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/260,190
; FILING DATE: 15-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863
; REFERENCE/DOCKET NUMBER: D-0021.3D
; TELEPHONE: 415-435-2034
; TELEFAX: 415-435-0727
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1522 base pairs
; TYPE: nucleic acid

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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-477-504A-1.

Query Match 100.0%; Score 1522; DB 2; Length 1522;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACAGTCAGCGCATGGCTCCCTGTGCCCCAGCCCCCTGGCTCCCTCTGTGATCCCGGCC 60
Db 1 ACAGTCAGCGCATGGCTCCCTGTGCCCCAGCCCCCTGGCTCCCTCTGTGATCCCGGCC 60
QY 61 CCTGCTCCAGGCCTCACTGTGCAACTGCTGTCTACTGCTGCTTCTGATGCCCTGCCAT 120
Db 61 CCTGCTCCAGGCCTCACTGTGCAACTGCTGTCTACTGCTGCTTCTGATGCCCTGCCAT 120
QY 121 CCCCAGAGGTTGCCCCGGGATGCAGGAGGATTCCTCCCTTGGGAGGAGGCTCTTCTGGGAA 180
Db 121 CCCCAGAGGTTGCCCCGGGATGCAGGAGGATTCCTCCCTTGGGAGGAGGCTCTTCTGGGAA 180
QY 181 GATGACCCACTGGGCGAGGAGGATCTGCCCCAGTGAAGAGGATTCACCCAGAGAGGAGAT 240
Db 181 GATGACCCACTGGGCGAGGAGGATCTGCCCCAGTGAAGAGGATTCACCCAGAGAGGAGAT 240
QY 241 CCACCCGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGATCTACCT 300
Db 241 CCACCCGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGATCTACCT 300
QY 301 GAAGTTAAGCCTAAATCAGAAGAGAGGGCTCCCTGAAGTTAGAGGATCTACCTACTGTT 360
Db 301 GAAGTTAAGCCTAAATCAGAAGAGAGGGCTCCCTGAAGTTAGAGGATCTACCTACTGTT 360
QY 361 GAGGCTCCTGAGATCCTCAAGAACCCAGAAATATGCCACAGGGACAAAGAGGGAT 420
Db 361 GAGGCTCCTGAGATCCTCAAGAACCCAGAAATATGCCACAGGGACAAAGAGGGAT 420
QY 421 GACCAGATCATTGGCGCTATGGAGGCGACCCCGCTGGCCCGGGGTGTCCCCAGCTGC 480
Db 421 GACCAGATCATTGGCGCTATGGAGGCGACCCCGCTGGCCCGGGGTGTCCCCAGCTGC 480
QY 481 GCGGGCCGCTTCCAGTCCCGGTGATATCCGCCGCCAGCTCGCCGCCCTTCTGCCCCGCC 540
Db 481 GCGGGCCGCTTCCAGTCCCGGTGATATCCGCCGCCAGCTCGCCGCCCTTCTGCCCCGCC 540
QY 541 CTGCGCCCTTGGAACTCCTGGCTTCCAGCTCCCGCCGCTCCAGAACTGCGCTCGCGC 600
Db 541 CTGCGCCCTTGGAACTCCTGGCTTCCAGCTCCCGCCGCTCCAGAACTGCGCTCGCGC 600
QY 601 AACAAATGGCCACAGTGTGCAACTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
Db 601 AACAAATGGCCACAGTGTGCAACTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
QY 661 GGGCGGGAGTACCGGGCTCTGCAGCTGCTGCACTGCGGGGGCTGCAGGTGCTCGGGC 720
Db 661 GGGCGGGAGTACCGGGCTCTGCAGCTGCTGCACTGCGGGGGCTGCAGGTGCTCGGGC 720
QY 721 TCGGAGCACACTGTGGAAGGCCACCGTTTCCCTGCCGAGATCCACGTGTTTCACTCAGC 780
Db 721 TCGGAGCACACTGTGGAAGGCCACCGTTTCCCTGCCGAGATCCACGTGTTTCACTCAGC 780
QY 781 ACCGCCCTTTCAGAGTTGACGAGGCTTGGGGCGCCCGGGAGGCTTGGCCGCTGTGGCC 840
Db 781 ACCGCCCTTTCAGAGTTGACGAGGCTTGGGGCGCCCGGGAGGCTTGGCCGCTGTGGCC 840
QY 841 GCCTTCTGGAGAGGGCCCGGAGAAACAGTGCCTATGAGCAGTTGCTGCTGCTGCTG 900
Db 841 GCCTTCTGGAGAGGGCCCGGAGAAACAGTGCCTATGAGCAGTTGCTGCTGCTGCTG 900
QY 901 GAAGAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCCGAGGACTGGACATATCTGCACTC 960
Db 901 GAAGAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCCGAGGACTGGACATATCTGCACTC 960

RESULT 3
US-08-486-756A-1
; Sequence 1, Application US/08486756A
; Patent No. 5981711
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: 6 Mariposa Court
; CITY: Tiburon
; STATE: California
; COUNTRY: USA
; ZIP: 94920
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,756A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/260,190
; FILING DATE: 15-JUN-1994
; ATTORNEY/AGENT INFORMATION:

NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021.3C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-2034
TELEFAX: 415-435-0727
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1522 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-486-756A-1

Query Match 100.0%; Score 1522; DB 2; Length 1522;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACAGTCAGCCGCGATGGCTCCCTGTCGCCAGCCCTGGCTCCCTCTGTTGATCCCGGCC 60
Db 1 ACAGTCAGCCGCGATGGCTCCCTGTCGCCAGCCCTGGCTCCCTCTGTTGATCCCGGCC 60
Qy 61 CCTGTCCAGGCTCACTGTGCAACTGCTGCTGCTCACTGCTGCTTCTGATGCCTGTCCAT 120
Db 61 CCTGTCCAGGCTCACTGTGCAACTGCTGCTGCTCACTGCTGCTTCTGATGCCTGTCCAT 120
Qy 121 CCCAGAGGTTGCCCGGATGAGGAGGATTCCCTTGGGAGGAGGCTCTTCTGGGGAA 180
Db 121 CCCAGAGGTTGCCCGGATGAGGAGGATTCCCTTGGGAGGAGGCTCTTCTGGGGAA 180
Qy 181 GATGACCCACTGGGCGAGGAGGATCTGCCAGTGAAGAGGATTACCCAGAGAGGAGGAT 240
Db 181 GATGACCCACTGGGCGAGGAGGATCTGCCAGTGAAGAGGATTACCCAGAGAGGAGGAT 240
Qy 241 CCACCCGAGAGGAGGATCTACTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCT 300
Db 241 CCACCCGAGAGGAGGATCTACTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCT 300
Qy 301 GAAGTTAAGCCTAAATCAGAAAGAGGAGGCTCCCTGAAGTTAGAGGATCTACCTACTGTT 360
Db 301 GAAGTTAAGCCTAAATCAGAAAGAGGAGGCTCCCTGAAGTTAGAGGATCTACCTACTGTT 360
Qy 361 GAGGCTCTGGAGATCCTCAAGAACCCAGAAATATGCCCCACAGGGACAAAGAGGGAT 420
Db 361 GAGGCTCTGGAGATCCTCAAGAACCCAGAAATATGCCCCACAGGGACAAAGAGGGAT 420
Qy 421 GACAGAGTCATTGGCGCTATGAGGCGACCCGCTGGCCCCGGGTGTCCTCCAGCCTGC 480
Db 421 GACAGAGTCATTGGCGCTATGAGGCGACCCGCTGGCCCCGGGTGTCCTCCAGCCTGC 480
Qy 481 GCGGCGCGCTTCCAGTCCCGGTGGATATCCGCCCCCAGCTCGCCGCTTCTGCCCCGCC 540
Db 481 GCGGCGCGCTTCCAGTCCCGGTGGATATCCGCCCCCAGCTCGCCGCTTCTGCCCCGCC 540
Qy 541 CTGCGCCCGCTGGAACTCCTGGGCTTCCAGCTCCCGCGCTCCAGAACTGGCGCTGCGC 600
Db 541 CTGCGCCCGCTGGAACTCCTGGGCTTCCAGCTCCCGCGCTCCAGAACTGGCGCTGCGC 600
Qy 601 AACAAATGSCACAGTGTGCAACTGACCCCTGCTCCTGGGCTAGAGATGGCTTGGGTCCC 660
Db 601 AACAAATGSCACAGTGTGCAACTGACCCCTGCTCCTGGGCTAGAGATGGCTTGGGTCCC 660
Qy 661 GGGCGGGAGTACCGGGCTCTGAGCTGCATCTGCACTGGGGGGCTGCAGGTCTCGGGGC 720
Db 661 GGGCGGGAGTACCGGGCTCTGAGCTGCATCTGCACTGGGGGGCTGCAGGTCTCGGGGC 720
Qy 721 TCGGAGCACACTGTGGAAGGCCACCGTTTCCCTGCCGAGATCCAGTGGTTACCTCAGC 780
Db 721 TCGGAGCACACTGTGGAAGGCCACCGTTTCCCTGCCGAGATCCAGTGGTTACCTCAGC 780

Qy 781 ACCGCCCTTTGCCAGAGTTGACGAGGCCCTTGGGGCGCCCGGAGGCCCTGGCCCTGTTGGCC 840
Db 781 ACCGCCCTTTGCCAGAGTTGACGAGGCCCTTGGGGCGCCCGGAGGCCCTGGCCCTGTTGGCC 840
Qy 841 GCCTTTCTGGAGGAGGGCCCGGAAGAAAACAGTGCCTATGAGCAGTTGCTGTCTCGCTTG 900
Db 841 GCCTTTCTGGAGGAGGGCCCGGAAGAAAACAGTGCCTATGAGCAGTTGCTGTCTCGCTTG 900
Qy 901 GAAAGAAATCGCTGAGGAAGGCTCAGAGACTCAGAGTCCCAGGACTGACATATCTGCACTC 960
Db 901 GAAAGAAATCGCTGAGGAAGGCTCAGAGACTCAGAGTCCCAGGACTGACATATCTGCACTC 960
Qy 961 CTGCCCTCTGACTTTCAGCCGCTACTTCCAAATATGAGGGTCTCTGACTACACCCCTGT 1020
Db 961 CTGCCCTCTGACTTTCAGCCGCTACTTCCAAATATGAGGGTCTCTGACTACACCCCTGT 1020
Qy 1021 GCCCAGGGTGTCTATCTGACTGTGTTTAAACAGACAGTATGCTGAGTCTAAGCAGCTC 1080
Db 1021 GCCCAGGGTGTCTATCTGACTGTGTTTAAACAGACAGTATGCTGAGTCTAAGCAGCTC 1080
Qy 1081 CACACCCCTCTCTGACACCCCTGTGGGACCTGTGACTCTCGGCTACAGCTGAACCTCCGA 1140
Db 1081 CACACCCCTCTCTGACACCCCTGTGGGACCTGTGACTCTCGGCTACAGCTGAACCTCCGA 1140
Qy 1141 GCGACGAGCCTTTGAATGGGCGAGTGAATGAGGCCCTCTTCCCTGCTGGAGTGGACAGC 1200
Db 1141 GCGACGAGCCTTTGAATGGGCGAGTGAATGAGGCCCTCTTCCCTGCTGGAGTGGACAGC 1200
Qy 1201 AGTCCTCGGGCTGCTGAGCCAGTCCAGCTGAATTCCTGCTGGTGGTGAACATCCTA 1260
Db 1201 AGTCCTCGGGCTGCTGAGCCAGTCCAGCTGAATTCCTGCTGGTGGTGAACATCCTA 1260
Qy 1261 GCCCTGGTTTTCGCTCCTTTTGTCTGTCACACAGCGTCCGCTTCTTGTGAGATGAGA 1320
Db 1261 GCCCTGGTTTTCGCTCCTTTTGTCTGTCACACAGCGTCCGCTTCTTGTGAGATGAGA 1320
Qy 1321 AGGCAGCACAGAGGGGAACCAAGGGGGTGTGAGTACCGCCCCAGAGAGGTAGCCGAG 1380
Db 1321 AGGCAGCACAGAGGGGAACCAAGGGGGTGTGAGTACCGCCCCAGAGAGGTAGCCGAG 1380
Qy 1381 ACTGGAGCCTAGAGGCTGGATCTTGGAGAAATGTGAGAACCCAGCCAGAGGCATCTGAGG 1440
Db 1381 ACTGGAGCCTAGAGGCTGGATCTTGGAGAAATGTGAGAACCCAGCCAGAGGCATCTGAGG 1440
Qy 1441 GGAGCCGGTAACTGCTGCTGCTGCTCAATATGCCACTTCTTTAACTGCCAAGAAATT 1500
Db 1441 GGAGCCGGTAACTGCTGCTGCTGCTCAATATGCCACTTCTTTAACTGCCAAGAAATT 1500
Qy 1501 TTTTAAATAAATAATTATAAT 1522
Db 1501 TTTTAAATAAATAATTATAAT 1522

RESULT 4
US-08-485-862B-1
; Sequence 1, Application US/08485862B
; Patent No. 5989838
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: 6 Mariposa Court
; CITY: Tiburon
; STATE: California
; COUNTRY: USA
; ZIP: 94920
; COMPUTER READABLE FORM: Floppy disk
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,862B

FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/477,504
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:

NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021.3D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-2034
TELEFAX: 415-435-0727

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:

LENGTH: 1522 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO

US-08-485-862B-1

Query Match 100.0%; Score 1522; DB 2; Length 1522;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ACAGTCAGCCGATGGCTCCCTGTGCCCCAGCCCCCTGGCTCCCTCTGTTGATCCCGGCC	60
Db	1	ACAGTCAGCCGATGGCTCCCTGTGCCCCAGCCCCCTGGCTCCCTCTGTTGATCCCGGCC	60
QY	61	CCTGCTCCAGCCCTCACTGTGCAACTGCTGTCTGCTCACTGTCTGCTTCTGATGCCCTGTCCAT	120
Db	61	CCTGCTCCAGCCCTCACTGTGCAACTGCTGTCTGCTCACTGTCTGCTTCTGATGCCCTGTCCAT	120
QY	121	CCCCAGAGTTGCCCGGATGCAGGAGGATTCCTCCCTTGGGAGGAGGCTCTTCTGGGGAA	180
Db	121	CCCCAGAGTTGCCCGGATGCAGGAGGATTCCTCCCTTGGGAGGAGGCTCTTCTGGGGAA	180
QY	181	GATGACCCACTGGGCGAGGAGGATCTGCCCCAGTGAAGAGGATTCACCCAGAGAGGAGGAT	240
Db	181	GATGACCCACTGGGCGAGGAGGATCTGCCAGTGAAGAGGATTCACCCAGAGAGGAGGAT	240
QY	241	CCACCCGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCT	300
Db	241	CCACCCGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCT	300
QY	301	GAAGTTAAGCTAAATCAGAAGAACAGAGGGCTCCCTGAAGTTAGAGGATCTACCTACTGTT	360
Db	301	GAAGTTAAGCTAAATCAGAAGAACAGAGGGCTCCCTGAAGTTAGAGGATCTACCTACTGTT	360
QY	361	GAGGCTCCTGGAGATCCTCAAGAACCCCAAGATTAATGCCACAGGGACAAAGAGGGGAT	420
Db	361	GAGGCTCCTGGAGATCCTCAAGAACCCCAAGATTAATGCCACAGGGACAAAGAGGGGAT	420
QY	421	GACCAGAGTCATTGGCGCTATGGAGCGACCCGCTGGCCCCGGGTGTCCCCAGCCTGC	480
Db	421	GACCAGAGTCATTGGCGCTATGGAGCGACCCGCTGGCCCCGGGTGTCCCCAGCCTGC	480
QY	481	GCGGGCCGCTCCAGTCCCGGTGGATATCGCCCCCAGCTCGCCCGCTTCTGCCCGGCC	540
Db	481	GCGGGCCGCTCCAGTCCCGGTGGATATCGCCCCCAGCTCGCCCGCTTCTGCCCGGCC	540
QY	541	CTGCGCCCTCGGAACCTCCTGGGCTTCCAGCTCCCGCCGCTCCAGAACTCGCGCTGCGC	600
Db	541	CTGCGCCCTCGGAACCTCCTGGGCTTCCAGCTCCCGCCGCTCCAGAACTCGCGCTGCGC	600

QY	601	AACAATGGCCACAGTGTGCAACTGACCCCTGCCTCCTGGGCTAGAGATGGCTCTGGGTCCC	660
Db	601	AACAATGGCCACAGTGTGCAACTGACCCCTGCCTCCTGGGCTAGAGATGGCTCTGGGTCCC	660
QY	661	GGGCGGAGTACCGGGCTCTGAGCTGCATCTGCACCTGGGGGCTGCAGGTGCTCCGGC	720
Db	661	GGGCGGAGTACCGGGCTCTGAGCTGCATCTGCACCTGGGGGCTGCAGGTGCTCCGGC	720
QY	721	TCGGAGCACACTGTGAAGGCCACCGTTTCCCTGCCGAGATCCACGTGTTTCACTCAGC	780
Db	721	TCGGAGCACACTGTGAAGGCCACCGTTTCCCTGCCGAGATCCACGTGTTTCACTCAGC	780
QY	781	ACCGCCTTTGCCAGAGTTGACGAGGCCCTTGGGGCGCCCGGAGGCCCTGGCCGTGTTGCC	840
Db	781	ACCGCCTTTGCCAGAGTTGACGAGGCCCTTGGGGCGCCCGGAGGCCCTGGCCGTGTTGCC	840
QY	841	GCCTTTCTGGAGGAGGGCCCGGAGAAACAGTGCCTATGAGCAGTTGCTCTCGCTTG	900
Db	841	GCCTTTCTGGAGGAGGGCCCGGAGAAACAGTGCCTATGAGCAGTTGCTCTCGCTTG	900
QY	901	GAAGAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCCAGGACTGGACATATCTGCACTC	960
Db	901	GAAGAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCCAGGACTGGACATATCTGCACTC	960
QY	961	CTGCCCTCTGACTTCAGCCGCTACTTCCAATATGAGGGGTCTCTGACTACACCCGCTGT	1020
Db	961	CTGCCCTCTGACTTCAGCCGCTACTTCCAATATGAGGGGTCTCTGACTACACCCGCTGT	1020
QY	1021	GCCCAGGCTCATCTGGACTGTGTTTAAACCAGACAGTGTGATGCTGCTAAGCAGCTC	1080
Db	1021	GCCCAGGCTCATCTGGACTGTGTTTAAACCAGACAGTGTGATGCTGCTAAGCAGCTC	1080
QY	1081	CACACCCCTCTGTGACACCCCTGTGGGACCTGGTGACTCTCGGCTACAGCTGAACCTTCCGA	1140
Db	1081	CACACCCCTCTGTGACACCCCTGTGGGACCTGGTGACTCTCGGCTACAGCTGAACCTTCCGA	1140
QY	1141	GCGACGAGCCCTTGAATGGGCGAGTGATGAGGCCCTCCTTCCCTGCTGGAGTGGACAGC	1200
Db	1141	GCGACGAGCCCTTGAATGGGCGAGTGATGAGGCCCTCCTTCCCTGCTGGAGTGGACAGC	1200
QY	1201	AGTCTCGGGCTGTGAGCCAGTCCAGCTGAATTCCTGCTGGCTGGTGTGATGATCCTA	1260
Db	1201	AGTCTCGGGCTGTGAGCCAGTCCAGCTGAATTCCTGCTGGCTGGTGTGATGATCCTA	1260
QY	1261	GCCCTGTTTGGCCCTCCTTTTGTGCTGTCCAGCGTCCGCTTCTTGTGAGATGAGA	1320
Db	1261	GCCCTGTTTGGCCCTCCTTTTGTGCTGTCCAGCGTCCGCTTCTTGTGAGATGAGA	1320
QY	1321	AGGCAGACAGAGGGGAACCAAGGGGTGTGAGCTACCGCCAGCAGAGGTAGCCGAG	1380
Db	1321	AGGCAGACAGAGGGGAACCAAGGGGTGTGAGCTACCGCCAGCAGAGGTAGCCGAG	1380
QY	1381	ACTGAGCCTAGAGGCTGGATCTTGGAGAAATGTGAGAAAGCCAGAGGCATCTGAGGG	1440
Db	1381	ACTGAGCCTAGAGGCTGGATCTTGGAGAAATGTGAGAAAGCCAGAGGCATCTGAGGG	1440
QY	1441	GGAGCCGTTAACTGTCTGCTGCTCATTATGCCACTTCTTTAACTGCCAAGAAATT	1500
Db	1441	GGAGCCGTTAACTGTCTGCTGCTCATTATGCCACTTCTTTAACTGCCAAGAAATT	1500
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Db	1501	TTTTTAAATAAATATTTATAAT	1522

RESULT 5
US-08-787-739-1
; Sequence 1, Application US/08787739
; Patent No. 6027887
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir

TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: 369 Pine Street, Suite 610
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/787,739
FILING DATE: 24-JAN-1997
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/485,049
FILING DATE: 07-JUN-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/486,756
FILING DATE: 07-JUN-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/477,504
FILING DATE: 07-JUN-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/481,658
FILING DATE: 07-JUN-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/485,862
FILING DATE: 07-JUN-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/485,863
FILING DATE: 07-JUN-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/487,077
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021.4
TELEPHONE: 415-981-2034
TELEFAX: 415-981-0332
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1522 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO

US-08-787-739-1
Query Match 100.0%; Score 1522; DB 3; Length 1522;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACAGTCAGCCGATGGCTCCCTGTGCCCCAGCCCCCTGGCTCCCTCTGTTGATCCCGGCC 60
DB 1 ACAGTCAGCCGATGGCTCCCTGTGCCCCAGCCCCCTGGCTCCCTCTGTTGATCCCGGCC 60
QY 61 CCTGCTCAGGCCCTCACTGTGCAACTGCTGTGTCACTGCTGCTTCTGATGCTGTCCAT 120
DB 61 CCTGCTCAGGCCCTCACTGTGCAACTGCTGTGTCACTGCTGCTTCTGATGCTGTCCAT 120
QY 121 CCCCAGAGTTGCCCGGATGCAGGAGGATCCCCCTTGGGAGGAGGCTCTTCTGGGAA 180
DB 121 CCCCAGAGTTGCCCGGATGCAGGAGGATCCCCCTTGGGAGGAGGCTCTTCTGGGAA 180
QY 181 GATGACCCACTGGGCGGAGGAGGATCTGCCCACTGAAGAGGATTACCCAGAGAGGAGGAT 240

DB 181 GATGACCCACTGGGCGGAGGAGGATCTGCCCACTGAAGAGGATTACCCAGAGAGGAGGAT 240
QY 241 CCACCCGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCT 300
DB 241 CCACCCGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCT 300
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DB 301 GAAAGTTAAGCCTAATCAGAAAGAGAGGGCTCCCTGAAAGTTAGAGGATCTACCTACTGTT 360
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DB 361 GAGGCTCCTGGAGATCCTCAAGAACCCCAAGATAATGCCCCACAGGGACAAAGAGGGAT 420
QY 421 GACCAGAGTCAATTGGCGCTATGGAGGCGACCCGCGCTGGCCCCCGGGTGTCCCAGCCTGC 480
DB 421 GACCAGAGTCAATTGGCGCTATGGAGGCGACCCGCGCTGGCCCCCGGGTGTCCCAGCCTGC 480
QY 481 GCGGCGCGCTTCCAGTCCCGGTGGATATCCGCCCCCAGCTCGCGCTTGTGCCCGGCC 540
DB 481 GCGGCGCGCTTCCAGTCCCGGTGGATATCCGCCCCCAGCTCGCGCTTGTGCCCGGCC 540
QY 541 CTGCGCCCCCTGGAACCTCTGGGCTTCCAGTCCCGCGCTCCCAGAACTGGCCTGCGC 600
DB 541 CTGCGCCCCCTGGAACCTCTGGGCTTCCAGTCCCGCGCTCCCAGAACTGGCCTGCGC 600
QY 601 AACAAATGGCCACAGTGTGCAACTGACCCCTGCTTGGGCTAGAGATGGCTCTGGGTCCC 660
DB 601 AACAAATGGCCACAGTGTGCAACTGACCCCTGCTTGGGCTAGAGATGGCTCTGGGTCCC 660
QY 661 GGGCGGGAGTACCGGGCTCTGCAGCTGCATCTGCACTGGGGGCTGAGGTCTGCGGGC 720
DB 661 GGGCGGGAGTACCGGGCTCTGCAGCTGCATCTGCACTGGGGGCTGAGGTCTGCGGGC 720
QY 721 TCGGAGCACACTGTGAAGGCCACCGTTTCCCTGCCGAGATCCACGTGTTTACCTCAGC 780
DB 721 TCGGAGCACACTGTGAAGGCCACCGTTTCCCTGCCGAGATCCACGTGTTTACCTCAGC 780
QY 781 ACCGCTTTGCCAGAGTTGACGAGGCCCTTGGGGCGCCCGGAGGCCCTGCGCTGTTGGCC 840
DB 781 ACCGCTTTGCCAGAGTTGACGAGGCCCTTGGGGCGCCCGGAGGCCCTGCGCTGTTGGCC 840
QY 841 GCCTTTCTGGAGGAGGCCCGGAGAAACACAGTGCCTATGAGCAGTTGCTGCTCGCTTG 900
DB 841 GCCTTTCTGGAGGAGGCCCGGAGAAACACAGTGCCTATGAGCAGTTGCTGCTCGCTTG 900
QY 901 GAAGAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCCAGGACTGGACATATCTGCACCTC 960
DB 901 GAAGAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCCAGGACTGGACATATCTGCACCTC 960
QY 961 CTGCCCCCTGACTTCAAGCCGCTACTTCCAAATATGAGGGGTCTCTGACTACACCGCCCTGT 1020
DB 961 CTGCCCCCTGACTTCAAGCCGCTACTTCCAAATATGAGGGGTCTCTGACTACACCGCCCTGT 1020
QY 1021 GCCCAGGGTGTCTGAGTGTGTTTAAACCAGACAGTGTGCTGAGTGTAAAGCAGCTC 1080
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QY 1081 CACACCCCTCTCTGACACCCCTGTGGGACCTGTGACTCTCGGCTACAGCTGAACCTTCCGA 1140
DB 1081 CACACCCCTCTCTGACACCCCTGTGGGACCTGTGACTCTCGGCTACAGCTGAACCTTCCGA 1140
QY 1141 GCGACGCAGCCTTTGAATGGGCGAGTGAATTGAGGCCCTCTTCCCTGCTGGAGTGGACAGC 1200
DB 1141 GCGACGCAGCCTTTGAATGGGCGAGTGAATTGAGGCCCTCTTCCCTGCTGGAGTGGACAGC 1200
QY 1201 AGTCTCTGGGCTGTGAGCCAGTCCAGCTGAATTCCTGCTGGCTGTGGTGACATCCTA 1260
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QY 1261 GGCCTGGTTTTTGGCCTCTTTTGTGTGTACACAGCGTTCGCTTCTGTGTCAGATGAGA 1320

Db 1261 GCCCTGGTTTTTGGCCCTCCTTTTTTGGCTGTCAACGAGCGTCGGGTTCTTGTGCAGATGAGA 1320
QY 1321 AGGCAGCACAGAAGGGGAACCAAGGGGTGTGAGCTACCGCCAGCAGAGGTAGCCGAG 1380
Db 1321 AGGCAGCACAGAAGGGGAACCAAGGGGTGTGAGCTACCGCCAGCAGAGGTAGCCGAG 1380
QY 1381 ACTGGAGCCTAGAGGCTGGATCTTGGAGAAATGTGAGAAGCCAGCCAGAGGCATCTGAGGG 1440
Db 1381 ACTGGAGCCTAGAGGCTGGATCTTGGAGAAATGTGAGAAGCCAGCCAGAGGCATCTGAGGG 1440
QY 1441 GGAGCCGGTAAGTCTCTGCTCATTTATGCGCACTTCCTTTTAACTGCGCAAGAAATT 1500
Db 1441 GGAGCCGGTAAGTCTCTGCTCATTTATGCGCACTTCCTTTTAACTGCGCAAGAAATT 1500
QY 1501 TTTTAAATAAATAATTATTAAT 1522
Db 1501 TTTTAAATAAATAATTATTAAT 1522

RESULT 6

US-08-487-077A-1
; Sequence 1, Application US/08487077A
; Patent No. 6069242
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: 6 Mariposa Court
; CITY: Tiburon
; STATE: California
; COUNTRY: USA
; ZIP: 94920
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,077A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/260,190
; FILING DATE: 15-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863
; REFERENCE/DOCKET NUMBER: D-0021.3H
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-435-2034
; TELEFAX: 415-435-0727
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1522 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-487-077A-1

Query Match 100.0%; Score 1522; DB 3; Length 1522;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACAGTCAGCCGCGATGGCTCCCTGTGCCCCAGCCCTGGCTCCCTCTGTGATCCCGGCC 60
Db 1 ACAGTCAGCCGCGATGGCTCCCTGTGCCCCAGCCCTGGCTCCCTCTGTGATCCCGGCC 60

QY 61 CCTGCTCAGGCGCTCACTGTGCAACTGCTGCTGTCACTGCTGCTTCTGTATGCCTGTCCAT 120
Db 61 CCTGCTCAGGCGCTCACTGTGCAACTGCTGCTGTCACTGCTGCTTCTGTATGCCTGTCCAT 120
QY 121 CCCAGAGGTTGCCCGGATGAGGAGGATTCCCCCTTTGGAGGAGGCTCTTCTGGGGAA 180
Db 121 CCCAGAGGTTGCCCGGATGAGGAGGATTCCCCCTTTGGAGGAGGCTCTTCTGGGGAA 180
QY 181 GATGACCCACTGGGCGAGGAGGATCTGCCCCAGTGAAGAGGATTCAACCAGAGAGGAGAT 240
Db 181 GATGACCCACTGGGCGAGGAGGATCTGCCAGTGAAGAGGATTCAACCAGAGAGGAGAT 240
QY 241 CCACCCGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCT 300
Db 241 CCACCCGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCT 300
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QY 601 AACAAATGGCCACAGTGTGCAACTGACCTGCCTCCTGGGCTAGAGATGGCTCTGGGTCCC 660
Db 601 AACAAATGGCCACAGTGTGCAACTGACCTGCCTCCTGGGCTAGAGATGGCTCTGGGTCCC 660
QY 661 GGGCGGAGTACCGGGCTCTGCACTGCACTGTGCACTGGGGGCTGCAGGTCTGCCGGC 720
Db 661 GGGCGGAGTACCGGGCTCTGCACTGCACTGTGCACTGGGGGCTGCAGGTCTGCCGGC 720
QY 721 TCGGAGCACACTGTGAAGGCCACCGTTCCCTGCCGAGATCCAGTGGTTCACTCAGC 780
Db 721 TCGGAGCACACTGTGAAGGCCACCGTTCCCTGCCGAGATCCAGTGGTTCACTCAGC 780
QY 781 ACCGCCCTTTCAGAGTTGACGAGGCTTGGGGCGCCCGGAGGCTTGGCCGTGTTGGCC 840
Db 781 ACCGCCCTTTCAGAGTTGACGAGGCTTGGGGCGCCCGGAGGCTTGGCCGTGTTGGCC 840
QY 841 GCCTTTCTGGAGGAGGGCCCGGAAGAAACAGTGCCTATGAGCAGTTGCTGCTCGCTTG 900
Db 841 GCCTTTCTGGAGGAGGGCCCGGAAGAAACAGTGCCTATGAGCAGTTGCTGCTCGCTTG 900
QY 901 GAAGAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCCAGGACTGGACATATCTGCATC 960
Db 901 GAAGAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCCAGGACTGGACATATCTGCATC 960
QY 961 CTGCCCTCTGACTTCAGCCGCTACTTCCAATATGAGGGGTCTCTGACTACACCCCTGT 1020
Db 961 CTGCCCTCTGACTTCAGCCGCTACTTCCAATATGAGGGGTCTCTGACTACACCCCTGT 1020
QY 1021 GCCCAGGGTGTCACTGAGTGTGTTTAAACAGACAGTGTGCTGAGTGTGCTAAGCAGCTC 1080
Db 1021 GCCCAGGGTGTCACTGAGTGTGTTTAAACAGACAGTGTGCTGAGTGTGCTAAGCAGCTC 1080
QY 1081 CACACCCCTCTGTGACACCCCTGTGGGGACCTGGTGACTCTCGGCTACAGCTGAACCTCCGA 1140
Db 1081 CACACCCCTCTGTGACACCCCTGTGGGGACCTGGTGACTCTCGGCTACAGCTGAACCTCCGA 1140

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Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1201 AGTCCTCGGGCTGCTGAGCCAGTCCAGCTGAATTCCTGCTGGCTGGCTGCTGACATCCTA 1260
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1261 GCCCTGGTTTTTGGCCTCCTTTTGTGTCACCCAGCGTCGCGTTCCCTTGTGAGATGAGA 1320
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1321 AGGACACAGAAGGGGAACCAAGGGGGTGTGAGCTACCGCCCAGCAGAGGTAGCCGAG 1380
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1381 ACTGGAGCTAGAGGCTGGATCTTGGAGAAATGTGAGAGCCAGCCAGAGGATCTGAGGG 1440
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1441 GGAGCCGTAACCTGCTCCTGCTCATTAATGCCCACCTTCTTTAACTGCCAAGAAATT 1500
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1501 TTTTAAATAAATAATTTATAAT 1522
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1501 TTTTAAATAAATAATTTATAAT 1522

RESULT 7

US-08-485-863A-1
; Sequence 1, Application US/08485863A
; Patent No. 6093548
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: 6 Mariposa Court
; CITY: Tiburon
; STATE: California
; COUNTRY: USA
; ZIP: 94920
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,863A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/260,190
; FILING DATE: 15-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863
; REFERENCE/DOCKET NUMBER: D-0021.3G
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-435-2034
; TELEFAX: 415-435-0727
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1522 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO

; ANTI-SENSE: NO
US-08-485-863A-1
Query Match 100.0%; Score 1522; DB 3; Length 1522;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 61 CCTGCTCCAGGCCTCACTGTGCAACTGCTGCTGCTCACTGCTGCTTCTGATGCCTGTCCAT 120
Db CCTGCTCCAGGCCTCACTGTGCAACTGCTGCTGCTCACTGCTGCTTCTGATGCCTGTCCAT 120
QY 121 CCCACAGAGTTGCCCGGATGCAGAGGATTCCTCCCTTGGGAGGAGGCTCTTCTGGGAA 180
Db CCCACAGAGTTGCCCGGATGCAGAGGATTCCTCCCTTGGGAGGAGGCTCTTCTGGGAA 180
QY 181 GATGACCCACTGCGGAGGAGGATCTGCCCCAGTGAAGAGGATTCACCCAGAGAGGAGGAT 240
Db GATGACCCACTGCGGAGGAGGATCTGCCCCAGTGAAGAGGATTCACCCAGAGAGGAGGAT 240
QY 241 CCACCCGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCT 300
Db CCACCCGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCT 300
QY 301 GAAGTTAAGCCTAAATCAGAAGAGAGGCTCCCTGAAAGTTAGAGGATCTACCTACTGTT 360
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QY 361 GAGGCTCCTGGAGATCCTCAAGAACCCAGAAATATGCCACAGGGACAAAGAGGGGAT 420
Db GAGGCTCCTGGAGATCCTCAAGAACCCAGAAATATGCCACAGGGACAAAGAGGGGAT 420
QY 421 GACCAGAGTCATTGGCGCTATGGAGGCGACCCGCCCTTGGCCCGGGGTGCCCCAGCTGC 480
Db GACCAGAGTCATTGGCGCTATGGAGGCGACCCGCCCTTGGCCCGGGGTGCCCCAGCTGC 480
QY 481 GCGGCGCGCTTCCAGTCCCGGTGGATATCCGCCCCCAGCTCGCCGCTTCTGCCCCGGCC 540
Db GCGGCGCGCTTCCAGTCCCGGTGGATATCCGCCCCCAGCTCGCCGCTTCTGCCCCGGCC 540
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QY 721 TCGGAGCACACTGTGGAAGGCCACCGTTTCCCTGCCGAGATCCACGTGGTTTCCCTCAGC 780
Db TCGGAGCACACTGTGGAAGGCCACCGTTTCCCTGCCGAGATCCACGTGGTTTCCCTCAGC 780
QY 781 ACCGCTTTGCCAGAGTTGACGAGGCTTGGGGGCCCGGGAGGCTGGCCGTGTGGCC 840
Db ACCGCTTTGCCAGAGTTGACGAGGCTTGGGGGCCCGGGAGGCTGGCCGTGTGGCC 840
QY 841 GCCTTTCTGGAGGAGGGCCCGGAAGAAACAGTGCCTATGAGCAGTTGTCTCGCTTG 900
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QY 901 GAAGAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCCAGGACTGGACATATCTGCACTC 960
Db GAAGAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCCAGGACTGGACATATCTGCACTC 960
QY 961 CTGCCCCCTGACTTTCAGCCGCTACTTCCAATATGAGGGGTCTCTGACTACACCGCCTGT 1020
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Db 1021 GCCAGGGTGTATCTGGACTGTGTTTAAACAGACAGTGTGAGTGTCTAAGCAGCTC 1080
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Db 1081 CACACCTCTCTGACACCCCTGTGGGACCTGGTGTGACTCTCGGTACAGCTGAACCTCCGA 1140
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Db 1501 TTTTAAATAAATATTTTATAAT 1522

RESULT 8

US-08-485-049D-1
; Sequence 1, Application US/08485049D
; Patent No. 6204370
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: 369 Pine Street
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,049D
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/260,190
; FILING DATE: 15-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863
; REFERENCE/DOCKET NUMBER: D-0021.3E
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-981-2034
; TELEFAX: 415-981-0332
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1522 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-485-049D-1

Query Match 100.0%; Score 1522; DB 3; Length 1522;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACAGTCAGCCGCTGCTCCCTGTGCCCCAGCCCCCTGGCTCCCTCTGTGTGATCCCGGCC 60
Db 1 ACAGTCAGCCGCTGCTCCCTGTGCCCCAGCCCCCTGGCTCCCTCTGTGTGATCCCGGCC 60
QY 61 CCTGCTCCAGGCTCACTGTGCAACTGCTGTCTGCTGTCTGCTGTCTGATGCTGCTGCT 120
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QY 181 GATGACCCACTGGCGGAGGAGGATCTGCCAGTGAAGAGGATTCACCCAGAGAGGAGAT 240
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QY 241 CCACCCGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCT 300
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QY 301 GAAGTTAAGCTTAATCAGAAGAGAGGAGGCTCCCTGAAGTTAGAGGATCTACCTACTGTT 360
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QY 361 GAGGCTCTCTGGAGATCCTCAAGAAACCCAGAAATATGCCACAGGGACAAAGAGGGAT 420
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QY 421 GACCAGAGTATGGCGTATGAGGCGGACCCGCCCTGGCCCCGGGTGTCCCCAGCCTGC 480
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QY 481 GCGGGCCGCTTCCAGTCCCGGTGGATATCCGCCCCAGCTCCGCCCTTCTGCCCCGCC 540
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QY 601 AACATGSCCAGTGTGCAACTGACCTGCTCCCTGSGCTAGAGATGGCTCTGGGTCCC 660
Db 601 AACATGSCCAGTGTGCAACTGACCTGCTCCCTGSGCTAGAGATGGCTCTGGGTCCC 660
QY 661 GGGGGGAGTACCGGGCTCTGAGCTGCATCTGCACTGGGGGGCTGCAGGTCTGCGGGC 720
Db 661 GGGGGGAGTACCGGGCTCTGAGCTGCATCTGCACTGGGGGGCTGCAGGTCTGCGGGC 720
QY 721 TCGGAGCACACTGTGAAGGCCACCGTTTCCCTGCCGAGATCCACGTGTTTACCTCAGC 780
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QY 781 ACCGCTTTTCCAGAGTTGACAGGCGCTTGGGGCGCCCGGAGGCGCTGGCCGTTGGCC 840
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QY 841 GCCTTCTTGAGAGGGCCCGAAGAAAACAGTGCCTATGAGCAGTTGCTGTCTCGCTTG 900
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QY 1081 CACACCTCTCTGACACCTGTGGGGACCTGGTGACTCTCGGCTACAGTGAACTTCCGA 1140
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QY 1141 GCGACGAGCCTTTGAATGGGAGTGATTGAGGCCTCTTCCCCTGCTGAGTGGACAGC 1200
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QY 1201 AGTCCTCGGGCTGTGAGCCAGTCCAGCTGAATTCCTGCTGGCTGCTGTGACATCCTA 1260
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QY 1501 TTTTAAATAAATATTATAAT 1522
Db |||||

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US-09-178-115-1
; Sequence 1, Application US/09178115
; Patent No. 6297041
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; FILE REFERENCE: D-0021.5A
; CURRENT APPLICATION NUMBER: US/09/178,115
; CURRENT FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: 09/177,776
; EARLIER FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: 08/787,739
; EARLIER FILING DATE: 1997-01-24
; EARLIER APPLICATION NUMBER: 08/485,049
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/486,756
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/477,504
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/481,658
; EARLIER FILING DATE: 1995-06-07

; EARLIER APPLICATION NUMBER: 08/485,862
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/485,863
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/487,077
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/260,190
; EARLIER FILING DATE: 1994-06-15
; EARLIER APPLICATION NUMBER: 08/177,093
; EARLIER FILING DATE: 1993-12-30
; EARLIER APPLICATION NUMBER: 07/964,589
; EARLIER FILING DATE: 1992-10-21
; EARLIER APPLICATION NUMBER: PV-709-92
; EARLIER FILING DATE: 1992-03-11
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1522
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (13)..(1389)
; FEATURE:
; NAME/KEY: mat peptide
; LOCATION: (124)..(1389)
US-09-178-115-1

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 121 CCCAGAGGTTGCCCGGATGCAGGAGGATTCGCCCTTGGGAGGAGGCTTTCTTGGGGAA 180
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QY 181 GATGACCCACTGGCGAGGAGGATCTGCCAGTGAAGAGGATTCACCCAGAGAGGAGGAT 240
Db |||||
QY 241 CCACCCGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCT 300
Db |||||
QY 301 GAAGTTAAGCCTAAATCAGAAGAAGAGGGCTCCCTGAAGTTAGAGGATCTACCTACTGTT 360
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QY 421 GACCAGAGTCATTGGCGCTATGGAGGCGACCCGCCCTGGCCCCGGGTGTCCCAGCCTGC 480
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QY 481 GCGGCGCGCTTCCAGTCCCGGTGGATATCCGCCCGCCAGCTCGCCGCTTCTGCCCCGCC 540
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Db |||||
QY 601 AACAAATGGCCACAGTGTGCAACTGACCCCTGCTGGGCTAGAGATGGCTCTGGGTCCC 660

QY 421 GACCAGAGTCATTGGCGCTATGAGGCGACCCGCCCTGGCCCCCGGGTGTCCTCCAGCCTGC 480
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QY 781 ACCGCTTTGCCAGAGTTGACGAGGCTTGGGGCGCCCGGAGGCTGGCGCTGTGGCC 840
Db |||||
QY 781 ACCGCTTTGCCAGAGTTGACGAGGCTTGGGGCGCCCGGAGGCTGGCGCTGTGGCC 840
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QY 841 GCCTTTCTGGAGGAGGGCCCCGGAAGAAAACAGTGCCTATGAGCAGTTGCTGTCTCGTTG 900
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; Patent No. 6004535
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: Methods to Detect and Quantify MN Protein/Polypeptide
; TITLE OF INVENTION: Using MN-Specific Antibodies
; FILE REFERENCE: D-0021A
; CURRENT APPLICATION NUMBER: US/08/335,469A
; CURRENT FILING DATE: 1994-11-07
; EARLIER APPLICATION NUMBER: 07/964,589
; EARLIER FILING DATE: 1992-10-21
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1399
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1266)
US-08-335-469-1

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1399; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db |||||
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Db |||||
QY 121 CCGGAGAGGAGGATCTACCTGGAGAGGAGGCTCCCTGAAGTTAGAGGATCTACCTGAA 180
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QY 181 GTTAAAGCCTAAATCAGAAGAAAGAGGGCTCCCTGAAGTTAGAGGATCTACCTACTGTTGAG 240
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; Patent No. 5972353
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: 6 Mariposa Court
; CITY: Tiburon
; STATE: California
; COUNTRY: USA
; ZIP: 94920
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,504A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/260,190
; FILING DATE: 15-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863
; REFERENCE/DOCKET NUMBER: D-0021.3D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-435-2034
; TELEFAX: 415-435-0727
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10898 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-477-504A-5

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Qy	301	GAAAGTTAAGCCTAAATCAGAAAGAGAGGGCTCCCTGAAGTTAGAGGATCTACCTACTGTT	360
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Search completed: May 11, 2004, 16:37:36
Job time : 139 secs

GenCore version 5.1.6
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OMnucleic - nucleic search, using sw model

Run on: May 11, 2004, 13:34:08 ; Search time 694 Seconds
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Perfect score: 1522

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2941586 seqs, 2264995651 residues

Total number of hits satisfying chosen parameters: 5883172

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1522	100.0	1552	9	US-09-954-456-89
4	1522	100.0	1552	9	US-09-954-456-726
5	1522	100.0	1552	10	US-09-960-706-1080
6	1522	100.0	1552	10	US-09-873-367C-516
7	1522	100.0	1552	13	US-10-342-887-574
8	1522	100.0	1552	13	US-10-172-118-574
9	1522	100.0	1552	13	US-10-388-360-291
10	1522	100.0	1552	15	US-10-301-822-11
11	1522	100.0	1552	16	US-10-465-572-9
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13	1522	100.0	1552	16	US-10-295-027-1022
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15	1379.8	90.7	1833	9	US-09-783-708-2	Sequence 2, Appli
16	414.4	27.2	10898	9	US-09-772-719-5	Sequence 5, Appli
17	414.4	27.2	10898	10	US-09-967-237-5	Sequence 5, Appli
18	413.4	27.2	415	9	US-09-772-719-28	Sequence 28, Appl
19	413.4	27.2	445	10	US-09-967-237-28	Sequence 28, Appl
20	331	21.7	331	13	US-10-085-783A-11940	Sequence 11940, A
21	331	21.7	331	16	US-10-242-535A-11940	Sequence 11940, A
22	300.8	19.8	304	9	US-09-777-564-348	Sequence 348, App
23	300.8	19.8	304	15	US-10-015-219-348	Sequence 348, App
24	297	19.5	297	9	US-09-777-564-592	Sequence 592, App
25	297	19.5	297	15	US-10-015-219-592	Sequence 592, App
26	296	19.4	296	15	US-10-102-524-697	Sequence 697, App
27	293	19.3	305	9	US-09-777-564-8	Sequence 8, Appli
28	293	19.3	305	15	US-10-015-219-8	Sequence 8, Appli
29	277	18.2	277	15	US-10-102-524-453	Sequence 453, App
30	277	18.2	277	15	US-10-102-524-1020	Sequence 1020, Ap
31	275.4	18.1	277	15	US-10-102-524-1139	Sequence 1139, Ap
32	265	17.4	276	15	US-10-102-524-1444	Sequence 1444, Ap
33	233.4	15.3	470	9	US-09-772-719-55	Sequence 55, Appl
34	233.4	15.3	470	10	US-09-967-237-55	Sequence 55, Appl
35	194	12.7	243	9	US-09-867-701-9969	Sequence 9969, Ap
36	191	12.5	191	9	US-09-772-719-38	Sequence 38, Appl
37	191	12.5	191	10	US-09-967-237-38	Sequence 38, Appl
38	180.4	11.9	1401	9	US-09-772-719-49	Sequence 49, Appl
39	180.4	11.9	1401	10	US-09-967-237-49	Sequence 49, Appl
40	171	11.2	171	9	US-09-772-719-30	Sequence 30, Appl
41	171	11.2	171	10	US-09-967-237-30	Sequence 30, Appl
42	158	10.4	158	9	US-09-772-719-34	Sequence 34, Appl
43	158	10.4	158	10	US-09-967-237-34	Sequence 34, Appl
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45	145	9.5	145	10	US-09-967-237-35	Sequence 35, Appl

ALIGNMENTS

RESULT 1

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; Patent No. US20020137910A1
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: 369 Pine Street
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/772,719
; FILING DATE: 30-JAN-2001
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,049
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/260,190
; FILING DATE: 15-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863
; REFERENCE/DOCKET NUMBER: D-0021.3E
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-981-2034

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; TELEFAX: 415-981-0332
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1522 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-09-772-719-1

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 181 GATGACCCACTGGCGGAGGAGGATCTGCCAGTGAAGAGGATTACCCAGAGAGGAGGAT 240

QY 241 CCACCCGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACTCTGGAGAGGAGGATCTACCT 300
DB 241 CCACCCGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACTCTGGAGAGGAGGATCTACCT 300

QY 301 GAAGTTAAGCCTAAATCAGAAGAAAGAGGCTCCCTGAACTTAGAGGATCTACCTACTGTT 360
DB 301 GAAGTTAAGCCTAAATCAGAAGAAAGAGGCTCCCTGAACTTAGAGGATCTACCTACTGTT 360

QY 361 GAGGCTCCTGGAGATCCTCAAGAACCCAGAGATTAATGCCCAAGGGACAAAGAGGGAT 420
DB 361 GAGGCTCCTGGAGATCCTCAAGAACCCAGAGATTAATGCCCAAGGGACAAAGAGGGAT 420

QY 421 GACCAGAGTCATTGGCGCTATGGAGGCGACCGCCCTGGCCCGGGGTGTCCCCAGCCTGC 480
DB 421 GACCAGAGTCATTGGCGCTATGGAGGCGACCGCCCTGGCCCGGGGTGTCCCCAGCCTGC 480

QY 481 GCGGGCCGCTTCCAGTCCCGGTGGATATCCGCCCGCCAGCTCCCGCCCTTCTGCCCCGCC 540
DB 481 GCGGGCCGCTTCCAGTCCCGGTGGATATCCGCCCGCCAGCTCCCGCCCTTCTGCCCCGCC 540

QY 541 CTGCGCCCCCTTGAACCTCTGGGCTTCCAGCTCCCGCGCTCCAGAACTGCGCCCTGCGC 600
DB 541 CTGCGCCCCCTTGAACCTCTGGGCTTCCAGCTCCCGCGCTCCAGAACTGCGCCCTGCGC 600

QY 601 AACAAATGGCCACAGTGTGCAACTGACCTGCCTCTCTGGGCTAGAGATGGCTCTGGGTCCC 660
DB 601 AACAAATGGCCACAGTGTGCAACTGACCTGCCTCTCTGGGCTAGAGATGGCTCTGGGTCCC 660

QY 661 GGGCGGGAGTACCGGGCTCTGCAGCTGCATCTGCACCTGGGGGCTGCAGGCTCGTCCGGGC 720
DB 661 GGGCGGGAGTACCGGGCTCTGCAGCTGCATCTGCACCTGGGGGCTGCAGGCTCGTCCGGGC 720

QY 721 TCGGAGCACACTGTGGAAGGCCACCGTTTCCCTGCCGAGATCCACGTGGTTCCACTCAGC 780
DB 721 TCGGAGCACACTGTGGAAGGCCACCGTTTCCCTGCCGAGATCCACGTGGTTCCACTCAGC 780

QY 781 ACCGCCCTTTCACAGATTGACGAGGCTTGGGGGCCCGCCGGGAGGCTGGCCGTGTGGCC 840
DB 781 ACCGCCCTTTCACAGATTGACGAGGCTTGGGGGCCCGCCGGGAGGCTGGCCGTGTGGCC 840

QY 841 GCCTTTCTGGAGAGGGGCCCGGAAAGAACAGTGCCTATGACAGATTGCTGTCTCGCTTG 900
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DB 841 GCCTTTCTGGAGAGGGCCCCGGAAGAAACAGTGCCTATGAGCAGTTGCTGTCTCGCTTG 900
QY 901 GAAGAAATCGCTGAGGAAGCTCAGAGACTCAGGTCCAGGACTGGACATATCTGCACTC 960
DB 901 GAAGAAATCGCTGAGGAAGCTCAGAGACTCAGGTCCAGGACTGGACATATCTGCACTC 960
QY 961 CTGCCCTCTGACTTCAGCCGCTACTTCCAATATAGAGGGTCTCTGACTACACCGCCCTGT 1020
DB 961 CTGCCCTCTGACTTCAGCCGCTACTTCCAATATAGAGGGTCTCTGACTACACCGCCCTGT 1020
QY 1021 GCCCAGGGTGTCTATCTGGACTGTGTTTAAACCAGACAGTGTGCTGAGTGTCTAAGCAGCTC 1080
DB 1021 GCCCAGGGTGTCTATCTGGACTGTGTTTAAACCAGACAGTGTGCTGAGTGTCTAAGCAGCTC 1080
QY 1081 CACACCTCTCTGACACACCCCTGTGGGACCTGGTACTCTCGGCTACAGCTGAACCTCCGA 1140
DB 1081 CACACCTCTCTGACACACCCCTGTGGGACCTGGTACTCTCGGCTACAGCTGAACCTCCGA 1140
QY 1141 GCGACGCGAGCCTTTGAATGGGCGAGTGAATGAGGCCTCCTTCCCTGTGGAGTGGACAGC 1200
DB 1141 GCGACGCGAGCCTTTGAATGGGCGAGTGAATGAGGCCTCCTTCCCTGTGGAGTGGACAGC 1200
QY 1201 AGTCCTCGGGCTGTGAGCCAGTCCAGCTGAATTCCTGCTGGCTGCTGGTGACATCCTA 1260
DB 1201 AGTCCTCGGGCTGTGAGCCAGTCCAGCTGAATTCCTGCTGGCTGCTGGTGACATCCTA 1260
QY 1261 GCCCTGGTTTTTGGCCTCCTTTTGTGCTGTCAACCAGCGTCCGTTCTTGTGCAGATGAGA 1320
DB 1261 GCCCTGGTTTTTGGCCTCCTTTTGTGCTGTCAACCAGCGTCCGTTCTTGTGCAGATGAGA 1320
QY 1321 AGGCAGCACAGAAGGGGAACCAAGGGGGTGTGAGCTACCGCCAGCAGAGGTAGCCGAG 1380
DB 1321 AGGCAGCACAGAAGGGGAACCAAGGGGGTGTGAGCTACCGCCAGCAGAGGTAGCCGAG 1380
QY 1381 ACTGGAGCTAGAGGCTGGATCTTGAGAGAAATGTGAGAGCCAGAGGCTCTGAGGG 1440
DB 1381 ACTGGAGCTAGAGGCTGGATCTTGAGAGAAATGTGAGAGCCAGAGGCTCTGAGGG 1440
QY 1441 GGAGCCGTAACCTGTCTCTCTGCTCATTTATGCCACTTCTTAACTGCCAAGAAAT 1500
DB 1441 GGAGCCGTAACCTGTCTCTCTGCTCATTTATGCCACTTCTTAACTGCCAAGAAAT 1500
QY 1501 TTTTAAATAAATAATTTATAAT 1522
DB 1501 TTTTAAATAAATAATTTATAAT 1522
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RESULT 2
US-09-967-237-1
; Sequence 1, Application US/09967237
; Publication No. US20030049828A1
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; FILE REFERENCE: D-0021.5B-2
; CURRENT APPLICATION NUMBER: US/09/967,237
; CURRENT FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 09/178,115
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1522
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (13)..(1389)
; NAME/KEY: mat_peptide
; LOCATION: (124)..(1389)
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US-09-967-237-1

Query Match		100.0%;	Score 1522;	DB 10;	Length 1522;
Best Local Similarity		100.0%;	Pred. No. 0;		
Matches 1522;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	ACAGTCAGCCGCGATGGCTCCCTGTGCCCCAGCCCCCTGGCTCCCTCTGTTGATCCCGGCC	60		
Db	1	ACAGTCAGCCGCGATGGCTCCCTGTGCCCCAGCCCCCTGGCTCCCTCTGTTGATCCCGGCC	60		
QY	61	CCTGCTCCAGGCGCTCACTGTGCAACTGCTGCTGTCACTGCTGCTTCTGATGCCCTGTCCAT	120		
Db	61	CCTGCTCCAGGCGCTCACTGTGCAACTGCTGCTGTCACTGCTGCTTCTGATGCCCTGTCCAT	120		
QY	121	CCCCAGAGTTGGCCCCCGGATGCAGGAGGATTCCTCCCTTGGGAGGAGCTCTTCTGCGGAA	180		
Db	121	CCCCAGAGTTGGCCCCCGGATGCAGGAGGATTCCTCCCTTGGGAGGAGCTCTTCTGCGGAA	180		
QY	181	GATGACCCACTGGCGGAGGAGGATCTGCCAGTGAAGAGGATTCACCCAGAGAGGAGAT	240		
Db	181	GATGACCCACTGGCGGAGGAGGATCTGCCAGTGAAGAGGATTCACCCAGAGAGGAGAT	240		
QY	241	CCACCCGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCT	300		
Db	241	CCACCCGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCT	300		
QY	301	GAAGTTAAGCCTAAATCAGAAGAAGAGGGCTCCCTGAAGTTAGAGGATCTACCTACTGTT	360		
Db	301	GAAGTTAAGCCTAAATCAGAAGAAGAGGGCTCCCTGAAGTTAGAGGATCTACCTACTGTT	360		
QY	361	GAGGCTCCTGGAGATCCTCAAGAACCCAGAAATAATGCCACAGGGACAAAGAGGGAT	420		
Db	361	GAGGCTCCTGGAGATCCTCAAGAACCCAGAAATAATGCCACAGGGACAAAGAGGGAT	420		
QY	421	GACCAGAGTCAATTGGCGCTATGGAGGCGACCCCGCTGGCCCGGGTGTCCCCAGCCTGC	480		
Db	421	GACCAGAGTCAATTGGCGCTATGGAGGCGACCCCGCTGGCCCGGGTGTCCCCAGCCTGC	480		
QY	481	GCGGGCGCTTCCAGTCCCGGTGGATATCCGCCGCCCGCTGCGCGCTTCTGCCCCGCC	540		
Db	481	GCGGGCGCTTCCAGTCCCGGTGGATATCCGCCGCCCGCTGCGCGCTTCTGCCCCGCC	540		
QY	541	CTGCGCCCCCTGGAACCTCCTGGCTTCCAGCTCCCGCGCTCCAGAACTGCGCCCTGCGC	600		
Db	541	CTGCGCCCCCTGGAACCTCCTGGCTTCCAGCTCCCGCGCTCCAGAACTGCGCCCTGCGC	600		
QY	601	AACAATGGCCACAGTGTGCAACTGACCTCGCTCTGGGCTAGAGATGGCTCTGGGTCCC	660		
Db	601	AACAATGGCCACAGTGTGCAACTGACCTCGCTCTGGGCTAGAGATGGCTCTGGGTCCC	660		
QY	661	GGGCGGAGTACCGGGCTCTGCAGCTGCATCTGCACTGGGGGTGCAGGTCTGTCGGGC	720		
Db	661	GGGCGGAGTACCGGGCTCTGCAGCTGCATCTGCACTGGGGGTGCAGGTCTGTCGGGC	720		
QY	721	TCGGAGCACACTGTGGAAGGCCACCGTTTCCCTGCCGAGATCCACGTGGTTCACTCAGC	780		
Db	721	TCGGAGCACACTGTGGAAGGCCACCGTTTCCCTGCCGAGATCCACGTGGTTCACTCAGC	780		
QY	781	ACCGCCTTTGCCAGAGTTGACGAGGCGCTTGGGGCGCCCGGGAGGCGCTGGCCGTGTTGCC	840		
Db	781	ACCGCCTTTGCCAGAGTTGACGAGGCGCTTGGGGCGCCCGGGAGGCGCTGGCCGTGTTGCC	840		
QY	841	GCCTTTCTGGAGGAGGCGCCGGAAGAAACAGTGCCTATGAGCAGTTGCTGTCTCGCTTG	900		
Db	841	GCCTTTCTGGAGGAGGCGCCGGAAGAAACAGTGCCTATGAGCAGTTGCTGTCTCGCTTG	900		
QY	901	GAAGAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCCAGGACTGGACATATCTGCACTC	960		
Db	901	GAAGAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCCAGGACTGGACATATCTGCACTC	960		
QY	961	CTGCCCTCTGACTTTCAGCCGCTACTTCCAATATGAGGGGTCTCTGACTACACCGCCCTGT	1020		
Db	961	CTGCCCTCTGACTTTCAGCCGCTACTTCCAATATGAGGGGTCTCTGACTACACCGCCCTGT	1020		

QY	1021	GCCAGGGTGTCTCATCTGGACTGTGTTTAAACCAGACAGTGATGCTGAGTGCTTAAGCAGCTC	1080
Db	1021	GCCAGGGTGTCTCATCTGGACTGTGTTTAAACCAGACAGTGATGCTGAGTGCTTAAGCAGCTC	1080
QY	1081	CACACCTCTCTGACACCCCTGTGGGGACCTGGTGACTCTCGGCTACAGCTGAACCTCCGA	1140
Db	1081	CACACCTCTCTGACACCCCTGTGGGGACCTGGTGACTCTCGGCTACAGCTGAACCTCCGA	1140
QY	1141	GCGACGCGCCTTTGAATGGCGAGTGATTGAGGCCCTCCTTCCCTGCTGGAGTGACAGC	1200
Db	1141	GCGACGCGCCTTTGAATGGCGAGTGATTGAGGCCCTCCTTCCCTGCTGGAGTGACAGC	1200
QY	1201	AGTCTCGGGCTGCTGAGCCAGTCCAGCTGAATTCCTGCCTGGCTGCTGGTGACATCCTA	1260
Db	1201	AGTCTCGGGCTGCTGAGCCAGTCCAGCTGAATTCCTGCCTGGCTGCTGGTGACATCCTA	1260
QY	1261	GCCCTGGTTTTTGGCCTCCTTTTGTGCTGCACCGCGTCCGCTTCTTGTGCAGATGAGA	1320
Db	1261	GCCCTGGTTTTTGGCCTCCTTTTGTGCTGCACCGCGTCCGCTTCTTGTGCAGATGAGA	1320
QY	1321	AGGACGACAGAAAGGGAAACAAAGGGGGTGTGAGTACCGCCACGACAGAGGTAGCCGAG	1380
Db	1321	AGGACGACAGAAAGGGAAACAAAGGGGGTGTGAGTACCGCCACGACAGAGGTAGCCGAG	1380
QY	1381	ACTGGAGCCTAGAGGCTGGATCTTGGAGAAATGTGAGAAAGCCAGCCAGAGGCATCTGAGG	1440
Db	1381	ACTGGAGCCTAGAGGCTGGATCTTGGAGAAATGTGAGAAAGCCAGCCAGAGGCATCTGAGG	1440
QY	1441	GGAGCCGGTAACTGTCTGTCTCTCATTTATGCCACTTCTCTTTAACTGCCAAGAAAT	1500
Db	1441	GGAGCCGGTAACTGTCTGTCTCTCATTTATGCCACTTCTCTTTAACTGCCAAGAAAT	1500
QY	1501	TTTTAAATAAATAATTTATAAT	1522
Db	1501	TTTTAAATAAATAATTTATAAT	1522

RESULT 3

US-09-954-456-89
; Sequence 89, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cance
; FILE REFERENCE: 689290-76
; CURRENT APPLICATION NUMBER: US/09/954,456
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/60/233,617
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,052
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,923
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,134
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,637
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,638
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,711
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,720
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,840
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,863
; NUMBER OF SEQ ID NOS: 2276
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 89
; LENGTH: 1552

; SEQ ID NO 726
; LENGTH: 1552
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-456-726

Query Match 100.0%; Score 1522; DB 9; Length 1552;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACAGTCAGCCGATGGCTCCCTGTGCCCCAGCCCCCTGGCTCCCTCTGTTGATCCCGGCC 60
Db 31 ACAGTCAGCCGATGGCTCCCTGTGCCCCAGCCCCCTGGCTCCCTCTGTTGATCCCGGCC 90

QY 61 CCTGCTCCAGGCTCACTGTGCAACTGCTGCTGTCACTGTGCTTCTGATGCCGTGCCAT 120
Db 91 CCTGCTCCAGGCTCACTGTGCAACTGCTGCTGTCACTGTGCTTCTGATGCCGTGCCAT 150

QY 121 CCCAGAGGTTGCCCGGATGCAGGAGGATTCCTCCCTTGGAGGAGGCTCTTCTGGGGAA 180
Db 151 CCCAGAGGTTGCCCGGATGCAGGAGGATTCCTCCCTTGGAGGAGGCTCTTCTGGGGAA 210

QY 181 GATGACCCACTGGGCGAGGAGGATCTGCCAGTGAAGAGGATTCAACCAGAGAGGAGAT 240
Db 211 GATGACCCACTGGGCGAGGAGGATCTGCCAGTGAAGAGGATTCAACCAGAGAGGAGAT 270

QY 241 CCACCCGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCT 300
Db 271 CCACCCGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCT 330

QY 301 GAAGTTAAGCTAAATCAGAAGAGAGGGCTCCCTGAAGTTAGAGGATCTACCTACTGTT 360
Db 331 GAAGTTAAGCTAAATCAGAAGAGAGGGCTCCCTGAAGTTAGAGGATCTACCTACTGTT 390

QY 361 GAGGCTCCTGAGATCCTCAAGAACCCAGAAATAATGCCACAGGGACAAAGAGGGGAT 420
Db 391 GAGGCTCCTGAGATCCTCAAGAACCCAGAAATAATGCCACAGGGACAAAGAGGGGAT 450

QY 421 GACCAGAGTCATTGGCGCTATGGAGGCGACCCGCCCTGGCCCGGGGTGTCCCCAGCCTGC 480
Db 451 GACCAGAGTCATTGGCGCTATGGAGGCGACCCGCCCTGGCCCGGGGTGTCCCCAGCCTGC 510

QY 481 GCGGGCCGCTTCAGTCCCGGCTGGATATCCGCCCCAGCTCGCCCGCTTCCTGCCCCGCC 540
Db 511 GCGGGCCGCTTCAGTCCCGGCTGGATATCCGCCCCAGCTCGCCCGCTTCCTGCCCCGCC 570

QY 541 CTGCGCCCTCGAACTCCTGGCTTCCAGCTCCCGCCGCTCCAGAACTGCGCTGCGC 600
Db 571 CTGCGCCCTCGAACTCCTGGCTTCCAGCTCCCGCCGCTCCAGAACTGCGCTGCGC 630

QY 601 AACAAATGGCACAGTGTGCAACTGACCTGCCTCTGCGGTGAGATGGCTCTGGGTCCC 660
Db 631 AACAAATGGCACAGTGTGCAACTGACCTGCCTCTGCGGTGAGATGGCTCTGGGTCCC 690

QY 661 GGGCGGAGTACCGGCTCTGCAGCTGCATCTGCATGCGGGCTGCAGGTGCTCGCGGC 720
Db 691 GGGCGGAGTACCGGCTCTGCAGCTGCATCTGCATGCGGGCTGCAGGTGCTCGCGGC 750

QY 721 TCGGAGCACACTGTGGAAGGCCACCGTTTCCCTGCCGAGATCCACGTGTTTCACTCAGC 780
Db 751 TCGGAGCACACTGTGGAAGGCCACCGTTTCCCTGCCGAGATCCACGTGTTTCACTCAGC 810

QY 781 ACCGCTTTGCCAGAGTTGACGAGGCTTGGGGCGCCCGGAGGCTTGGCCGTGTGGCC 840
Db 811 ACCGCTTTGCCAGAGTTGACGAGGCTTGGGGCGCCCGGAGGCTTGGCCGTGTGGCC 870

QY 841 GCCTTTCTGAGAGGGCCCGGAAGAAACAGTGCCTATGAGCAGTTGCTGTCTGCTTG 900
Db 871 GCCTTTCTGAGAGGGCCCGGAAGAAACAGTGCCTATGAGCAGTTGCTGTCTGCTTG 930

QY 901 GAAGAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCAGGACTGGACATATCTGCACCTC 960
Db 931 GAAGAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCAGGACTGGACATATCTGCACCTC 990

QY 961 CTGCCCTCTGACTTCAGCCGCTACTTCCAATATGAGGGGTCTCTGACTACACCGCCCTGT 1020
Db 991 CTGCCCTCTGACTTCAGCCGCTACTTCCAATATGAGGGGTCTCTGACTACACCGCCCTGT 1050

QY 1021 GCCCAGGGTGTCACTTGAGACTGTGTTTAAACCAGACAGTGAAGTGAAGCAGCTC 1080
Db 1051 GCCCAGGGTGTCACTTGAGACTGTGTTTAAACCAGACAGTGAAGTGAAGCAGCTC 1110

QY 1081 CACACCTCTCTGACACCCCTGTGGGACCTGGTGAATCTCGGTACAGCTGAACCTCCGA 1140
Db 1111 CACACCTCTCTGACACCCCTGTGGGACCTGGTGAATCTCGGTACAGCTGAACCTCCGA 1170

QY 1141 GCGACGCGCTTGAATGGCGAGTGAATGAGGCCCTCTTCCCTGCTGGAGTGGACAGC 1200
Db 1171 GCGACGCGCTTGAATGGCGAGTGAATGAGGCCCTCTTCCCTGCTGGAGTGGACAGC 1230

QY 1201 AGTCCTCGGGCTGCTGAGCCAGTCCAGCTGAATTCCTGCTGGCTGCTGGTGACATCCTA 1260
Db 1231 AGTCCTCGGGCTGCTGAGCCAGTCCAGCTGAATTCCTGCTGGCTGCTGGTGACATCCTA 1290

QY 1261 GGCCTGGTTTGGCCTCCTTTTGTGCTGTCACCAGCGTCGCGTTCCTTGTGCAGATGAGA 1320
Db 1291 GGCCTGGTTTGGCCTCCTTTTGTGCTGTCACCAGCGTCGCGTTCCTTGTGCAGATGAGA 1350

QY 1321 AGGCAGCACAGAAAGGGGAAACCAGGGGGTGTGAGCTACCGCCAGCAGAGGTAGCCGAG 1380
Db 1351 AGGCAGCACAGAAAGGGGAAACCAGGGGGTGTGAGCTACCGCCAGCAGAGGTAGCCGAG 1410

QY 1381 ACTGGAGCTAGAGGCTGGATCTTGGAGAATGTGAGAAAGCCAGCCAGAGGCATCTGAGGG 1440
Db 1411 ACTGGAGCTAGAGGCTGGATCTTGGAGAATGTGAGAAAGCCAGCCAGAGGCATCTGAGGG 1470

QY 1441 GGAGCCGGTAACTGTCTCTGCTGCTCATTATGCCACCTTCTTAACTGCCAAGAAATT 1500
Db 1471 GGAGCCGGTAACTGTCTCTGCTGCTCATTATGCCACCTTCTTAACTGCCAAGAAATT 1530

QY 1501 TTTTAAATAAATAATTTATAAT 1522
Db 1531 TTTTAAATAAATAATTTATAAT 1552

RESULT 5
US-09-960-706-1080
; Sequence 1080, Application US/09960706
; Publication No. US20030134280A1
; GENERAL INFORMATION:
; APPLICANT: Munger, William E.
; TITLE OF INVENTION: Identifying Drugs for and Diagnosis of Benign Prostatic Hyperplasia
; FILE REFERENCE: 44921-5029-01US
; CURRENT APPLICATION NUMBER: US/09/960,706
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 60/223,323
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 09/873,319
; PRIOR FILING DATE: 2001-06-05
; NUMBER OF SEQ ID NOS: 1124
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1080
; LENGTH: 1552
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20030134280A1 X66839
US-09-960-706-1080

Query Match 100.0%; Score 1522; DB 10; Length 1552;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACAGTCAGCCGATGGCTCCCTGTGCCCCAGCCCCCTGGCTCCCTCTGTTGATCCCGGCC 60

Db 31 ACAGTCAGCCGCAATGGCTCCCTGTGCCCCCAGCCCTGGCTCCCTCTGTGTGATCCCGGCC 90

Qy 61 CTGTCTCCAGGCTCACTGTGCAACTGTCTGTCACTGTCTGTCTGTCTGTCTGTCTGTCTCAT 120

Db 91 CTGTCTCCAGGCTCACTGTGCAACTGTCTGTCACTGTCTGTCTGTCTGTCTGTCTGTCTCAT 150

Qy 121 CCCAGAGGTTGCCCGGATGCAGGAGGATTCCTCCCTTGGGAGGAGGCTCTTCTGGGGAA 180

Db 151 CCCAGAGGTTGCCCGGATGCAGGAGGATTCCTCCCTTGGGAGGAGGCTCTTCTGGGGAA 210

Qy 181 GATGACCCACTGGGCGAGGAGGATCTGCCCACTGAAGAGGATTCACCCAGAGAGGAGAT 240

Db 211 GATGACCCACTGGGCGAGGAGGATCTGCCCACTGAAGAGGATTCACCCAGAGAGGAGAT 270

Qy 241 CCACCCGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCT 300

Db 271 CCACCCGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCT 330

Qy 301 GAAGTTAAGCCTAAATCAGAGAAAGAGGGCTCCCTGAAAGTTAGAGGATCTACCTACTGTT 360

Db 331 GAAGTTAAGCCTAAATCAGAGAAAGAGGGCTCCCTGAAAGTTAGAGGATCTACCTACTGTT 390

Qy 361 GAGGCTCTTGAGATCCTCAAGAACCCAGAAATATGCCACAGGGACAAAGAGGGAT 420

Db 391 GAGGCTCTTGAGATCCTCAAGAACCCAGAAATATGCCACAGGGACAAAGAGGGAT 450

Qy 421 GACCAGAGTCATTGGCGCTATGAGAGCGACCCGCCCTGGCCCCGGGTGTCCCGAGCCTGC 480

Db 451 GACCAGAGTCATTGGCGCTATGAGAGCGACCCGCCCTGGCCCCGGGTGTCCCGAGCCTGC 510

Qy 481 GCGGGCGCTTCCAGTCCCCCGTGGATATCCGCCCCCGAGCTCGCCGCTTCTGCCCCGGCC 540

Db 511 GCGGGCGCTTCCAGTCCCCCGTGGATATCCGCCCCCGAGCTCGCCGCTTCTGCCCCGGCC 570

Qy 541 CTGCGCCCCCTGGAATCCTGGGCTTCCAGTCCCGCGCTCCAGAACTGCGCCCTGCGC 600

Db 571 CTGCGCCCCCTGGAATCCTGGGCTTCCAGTCCCGCGCTCCAGAACTGCGCCCTGCGC 630

Qy 601 AACAAATGCCACAGTGTGCAACTGACCTGCTCTGCGGCTAGAGATGGCTCTGGGTCCC 660

Db 631 AACAAATGCCACAGTGTGCAACTGACCTGCTCTGCGGCTAGAGATGGCTCTGGGTCCC 690

Qy 661 GCGCGGAGTACCGGGCTCTGCAGCTGCATCTGCACTGGGGGCTGCAGTCTGTCGGGC 720

Db 691 GCGCGGAGTACCGGGCTCTGCAGCTGCATCTGCACTGGGGGCTGCAGTCTGTCGGGC 750

Qy 721 TCGGAGCACACTGTGGAAGGCCACCGTTTCCCTGCCGAGATCCACGTGTTTCACTCAGC 780

Db 751 TCGGAGCACACTGTGGAAGGCCACCGTTTCCCTGCCGAGATCCACGTGTTTCACTCAGC 810

Qy 781 ACCGCCCTTGCCAGAGTTGACGAGGCTTGGGGGCGCCCGGAGGCTGGCCGTGTTGGCC 840

Db 811 ACCGCCCTTGCCAGAGTTGACGAGGCTTGGGGGCGCCCGGAGGCTGGCCGTGTTGGCC 870

Qy 841 GCCTTTCTGGAGGAGGCGCCCGGAAGAAACAGTGCCTATGAGCAGTTGCTGTCTGCTTG 900

Db 871 GCCTTTCTGGAGGAGGCGCCCGGAAGAAACAGTGCCTATGAGCAGTTGCTGTCTGCTTG 930

Qy 901 GAAGAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCCGAGGACTGGACATATCTGCACTC 960

Db 931 GAAGAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCCGAGGACTGGACATATCTGCACTC 990

Qy 961 CTGCCCTCTGACTTCAGCCGCTACTTCCAATATGAGGGGTCTCTGACTACACGCCCTGT 1020

Db 991 CTGCCCTCTGACTTCAGCCGCTACTTCCAATATGAGGGGTCTCTGACTACACGCCCTGT 1050

Qy 1021 GCCCAGGGTGTCTATCTGGAATGTGTTTAAACCAGACAGTGTGCTGCTGCTAAGCAGCTC 1080

Db 1051 GCCCAGGGTGTCTATCTGGAATGTGTTTAAACCAGACAGTGTGCTGCTGCTAAGCAGCTC 1110

Qy 1081 CACACCCCTCTGTACACCCCTGTGGGACCTGGTGACTCTCGGCTACAGCTGAATTCCTCGA 1140

Db 1111 CACACCCCTCTGTACACCCCTGTGGGACCTGGTGACTCTCGGCTACAGCTGAATTCCTCGA 1170

Qy 1141 GCGACGCAGCCCTTGAATGGGCGAGTATTGAGGCCCTCTTCCCTGCTGGAGTGGACAGC 1200

Db 1171 GCGACGCAGCCCTTGAATGGGCGAGTATTGAGGCCCTCTTCCCTGCTGGAGTGGACAGC 1230

Qy 1201 AGTCTCGGGCTGCTGAGCCAGTCCAGCTGAATTCCTGCTGGCTGCTGGTGACATCCTA 1260

Db 1231 AGTCTCGGGCTGCTGAGCCAGTCCAGCTGAATTCCTGCTGGCTGCTGGTGACATCCTA 1290

Qy 1261 GCCCTGGTTTGTGGCCTCTCTTTTGTGCTGTCAACAGCGTGGCTTCTTGTGCAGATGAGA 1320

Db 1291 GCCCTGGTTTGTGGCCTCTCTTTTGTGCTGTCAACAGCGTGGCTTCTTGTGCAGATGAGA 1350

Qy 1321 AGGCAGCACAGAAGGGGAACCAAAGGGGTGTGAGCTACCGCCAGCAGAGGTAGCCGAG 1380

Db 1351 AGGCAGCACAGAAGGGGAACCAAAGGGGTGTGAGCTACCGCCAGCAGAGGTAGCCGAG 1410

Qy 1381 ACTGGAGCCTAGAGGCTGGATCTTGGAGAAATGTGAGAAAGCCAGCCAGAGGCTCTGAGGG 1440

Db 1411 ACTGGAGCCTAGAGGCTGGATCTTGGAGAAATGTGAGAAAGCCAGCCAGAGGCTCTGAGGG 1470

Qy 1441 GGAGCCGGTAACTGTCTGTCTCTCATTTATGCACTTCTTTTAACTGCCAAGAAAT 1500

Db 1471 GGAGCCGGTAACTGTCTGTCTCTCATTTATGCACTTCTTTTAACTGCCAAGAAAT 1530

Qy 1501 TTTTAAAAATAATATTTATAAT 1522

Db 1531 TTTTAAAAATAATATTTATAAT 1552

RESULT 6

US-09-873-367C-516
; Sequence 516, Application US/09873367C
; Publication No. US20030165839A1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
; APPLICANT: Soppet, Daniel
; APPLICANT: Endress, Gregory
; APPLICANT: Augustus, Meena
; APPLICANT: Ebner, Reinhard
; APPLICANT: Carter, Kenneth
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
; TITLE OF INVENTION: Signature Gene Sets
; FILE REFERENCE: 689290-64
; CURRENT APPLICATION NUMBER: US/09/873,367C
; CURRENT FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: U.S. 60/236,891
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: U.S. 60/236,842
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: U.S. 60/244,867
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: U.S. 60/245,084
; PRIOR FILING DATE: 2000-11-01
; NUMBER OF SEQ ID NOS: 1067
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 516
; LENGTH: 1552
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-873-367C-516

Query Match 100.0%; Score 1522; DB 10; Length 1552;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACAGTCAGCCGCAATGGCTCCCTGTGCCCCCAGCCCTGGCTCCCTCTGTGTGATCCCGGCC 60

Db 31 ACAGTCAGCCGCAATGGCTCCCTGTGCCCCCAGCCCTGGCTCCCTCTGTGTGATCCCGGCC 90

Qy 61 CTGTCTCCAGGCTCACTGTGCAACTGTCTGTCTGCTGCTGCTGCTTCTGATGCTGTCCAT 120

Db 91 CTGTCTCCAGGCTCACTGTGCAACTGTCTGTCTGCTGCTGCTTCTGATGCTGTCCAT 150

QY 121 CCGCAGAGGTTGCCCGGATGCAGGAGGATTCCCCCTTGGGAGGAGGCTCTTCTGGGGAA 180
Db |||||
QY 151 CCCAGAGGTTGCCCGGATGCAGGAGGATTCCCCCTTGGGAGGAGGCTCTTCTGGGGAA 210
Db |||||
QY 181 GATACCCACTGGGCGAGGAGGATCTGCCAGTGAAGAGGATTCAACCAGAGAGGAGAT 240
Db |||||
QY 211 GATACCCACTGGGCGAGGAGGATCTGCCAGTGAAGAGGATTCAACCAGAGAGGAGAT 270
Db |||||
QY 241 CCACCCGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCT 300
Db |||||
QY 271 CCACCCGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCT 330
Db |||||
QY 301 GAAGTTAAGCCTAATCAGAAGAAGAGGGCTCCCTGAAGTTAGAGGATCTACCTACTGTT 360
Db |||||
QY 331 GAAGTTAAGCCTAATCAGAAGAAGAGGGCTCCCTGAAGTTAGAGGATCTACCTACTGTT 390
Db |||||
QY 361 GAGGCTCCTGGAGATCCTCAAGAACCCCAAGATAATGCCCCACAGGGACAAAGAGGGAT 420
Db |||||
QY 391 GAGGCTCCTGGAGATCCTCAAGAACCCCAAGATAATGCCCCACAGGGACAAAGAGGGAT 450
Db |||||
QY 421 GACCAGAGTCAATTGGCGCTATGGAGGGCAGCCCGCCCTGGCCCCGGGTGTCCCCAGCCTGC 480
Db |||||
QY 451 GACCAGAGTCAATTGGCGCTATGGAGGGCAGCCCGCCCTGGCCCCGGGTGTCCCCAGCCTGC 510
Db |||||
QY 481 GCGGGCCGCTTCCAGTCCCGGTGGATATCGGCCCCCCAGCTCGCGCCCTTCTGCCCGGCC 540
Db |||||
QY 511 GCGGGCCGCTTCCAGTCCCGGTGGATATCGGCCCCCCAGCTCGCGCCCTTCTGCCCGGCC 570
Db |||||
QY 541 CTGCGCCCCCTGGAACTCCTGGGCTTCCAGTCCCGCCGCTCCCAAGAACTGCGCCTGGC 600
Db |||||
QY 571 CTGCGCCCCCTGGAACTCCTGGGCTTCCAGTCCCGCCGCTCCCAAGAACTGCGCCTGGC 630
Db |||||
QY 601 AACAAATGGCCACAGTGTGCAACTGACCCCTGCCTCCTGGGCTAGAGATGGCTCTGGGTCCC 660
Db |||||
QY 631 AACAAATGGCCACAGTGTGCAACTGACCCCTGCCTCCTGGGCTAGAGATGGCTCTGGGTCCC 690
Db |||||
QY 661 GGGCGGGAGTACCGGGCTCTGCAGCTGATCTGCACCTGGGGGCTGCAGGTCTGCCGGGC 720
Db |||||
QY 691 GGGCGGGAGTACCGGGCTCTGCAGCTGATCTGCACCTGGGGGCTGCAGGTCTGCCGGGC 750
Db |||||
QY 721 TCGGAGCACACTGTGGAAGGCCACCGTTTCCCTGCCGAGATCCAGTGGTTTCACTCAGC 780
Db |||||
QY 751 TCGGAGCACACTGTGGAAGGCCACCGTTTCCCTGCCGAGATCCACGTGGTTTCACTCAGC 810
Db |||||
QY 781 ACCGCCCTTGGCAGAGTTGACGAGGCCCTTGGGGCGCCCGGAGGCTTGGCCGTGTTGGCC 840
Db |||||
QY 811 ACCGCCCTTGGCAGAGTTGACGAGGCCCTTGGGGCGCCCGGAGGCTTGGCCGTGTTGGCC 870
Db |||||
QY 841 GCCTTTCTGGAGGAGGGCCCGGAAGAAACAGTGCCTATGAGCAGTTGCTGTCTCGCTTG 900
Db |||||
QY 871 GCCTTTCTGGAGGAGGGCCCGGAAGAAACAGTGCCTATGAGCAGTTGCTGTCTCGCTTG 930
Db |||||
QY 901 GAAGAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCCAGGACTGGACATATCTGCATCTC 960
Db |||||
QY 931 GAAGAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCCAGGACTGGACATATCTGCATCTC 990
Db |||||
QY 961 CTGCCCTCTGACTTTCAGCCCGTACTTCCAATATGAGGGGTCTCTGACTACACCGCCCTGT 1020
Db |||||
QY 991 CTGCCCTCTGACTTTCAGCCCGTACTTCCAATATGAGGGGTCTCTGACTACACCGCCCTGT 1050
Db |||||
QY 1021 GCCCAGGGGTGTCATCTGGACTGTGTTTAAACAGACAGTGTGCTGAGTGCTAAGCAGCTC 1080
Db |||||
QY 1051 GCCCAGGGGTGTCATCTGGACTGTGTTTAAACAGACAGTGTGCTGAGTGCTAAGCAGCTC 1110
Db |||||
QY 1081 CACACCTCTCTGACACCCCTGTGGGACCTTGGTACTCTCGGCTACAGCTGAACCTTCGGA 1140
Db |||||
QY 1111 CACACCTCTCTGACACCCCTGTGGGACCTTGGTACTCTCGGCTACAGCTGAACCTTCGGA 1170
Db |||||
QY 1141 GCGACGCAGCCTTTGAATGGGCGAGTGATTGAGGCCCTCCTTCCCTGCTGGAGTGACAGC 1200
Db |||||
QY 1171 GCGACGCAGCCTTTGAATGGGCGAGTGATTGAGGCCCTCCTTCCCTGCTGGAGTGACAGC 1230
Db |||||

QY 1201 AGTCTCGGGCTGCTGAGCCAGTCCAGCTGAATTCTGCCCTGGCTGGTGACATCCTA 1260
Db |||||
QY 1231 AGTCTCGGGCTGCTGAGCCAGTCCAGCTGAATTCTGCCCTGGCTGGTGACATCCTA 1290
Db |||||
QY 1261 GCCCTGTTTTTGGCCCTCCTTTTGTGCTGTCAACGCGTCCGCTTCTTGTGAGATGAGA 1320
Db |||||
QY 1291 GCCCTGTTTTTGGCCCTCCTTTTGTGCTGTCAACGCGTCCGCTTCTTGTGAGATGAGA 1350
Db |||||
QY 1321 AGGCAGCACAGAAGGGGAACCAAGGGGTTGTAGCTACCGCCCCAGAGAGGTAGCCGAG 1380
Db |||||
QY 1351 AGGCAGCACAGAAGGGGAACCAAGGGGTTGTAGCTACCGCCCCAGAGAGGTAGCCGAG 1410
Db |||||
QY 1381 ACTGGAGCCTAGAGGCTGGATCTTTGGAGATGTGAGAAAGCCAGCAGAGGCTCTGAGGG 1440
Db |||||
QY 1411 ACTGGAGCCTAGAGGCTGGATCTTTGGAGATGTGAGAAAGCCAGCAGAGGCTCTGAGGG 1470
Db |||||
QY 1441 GGAGCCGGTAACTGTCTGTCTGCTCATTTATGCCACTTCTTTTAACTGCCAAGAAATT 1500
Db |||||
QY 1471 GGAGCCGGTAACTGTCTGTCTGCTCATTTATGCCACTTCTTTTAACTGCCAAGAAATT 1530
Db |||||
QY 1501 TTTTAAATAAATAATTATAAT 1522
Db |||||
QY 1531 TTTTAAATAAATAATTATAAT 1552
Db |||||

RESULT 7

US-10-342-887-574
; Sequence 574, Application US/10342887
; Publication No. US20040058340A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter S.
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Christopher J.
; APPLICANT: Van 't Veer, Laura Johanna
; APPLICANT: Van de Vijver, Marc J.
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-188-999
; CURRENT APPLICATION NUMBER: US/10/342,887
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 60/298,918
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/380,710
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 10/172,118
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 574
; LENGTH: 1552
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-342-887-574

Query Match 100.0%; Score 1522; DB 13; Length 1552;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACAGTCAGCCGCATGGCTCCCTGTGCCAGCCCTGGCTCCCTCTGTTGATCCCGGCC 60
Db |||||
QY 31 ACAGTCAGCCGCATGGCTCCCTGTGCCAGCCCTGGCTCCCTCTGTTGATCCCGGCC 90
Db |||||
QY 61 CCTGCTCCAGGCTCACTGTGCAACTGTGCTGTCACTGTGCTTCTGATGCCGTGCCAT 120
Db |||||
QY 91 CCTGCTCCAGGCTCACTGTGCAACTGTGCTGTCACTGTGCTTCTGATGCCGTGCCAT 150
Db |||||
QY 121 CCCCAGAGGTTGCCCGGATGCAGGAGGATTCCCCCTTGGGAGGAGGCTTCTTCTGGGAA 180
Db |||||
QY 151 CCCCAGAGGTTGCCCGGATGCAGGAGGATTCCCCCTTGGGAGGAGGCTTCTTCTGGGAA 210
Db |||||
QY 181 GATGACCCACTGGGCGAGGAGGATCTGCCAGTGAAGAGGATTCAACCAGAGAGGAGAT 240
Db |||||

Db 211 GATGACCACTGGCGAGGAGGATCTGCCAGTGAAGAGGATTCAACCAGAGAGGAGGAT 270
Qy 241 CCACCCGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCT 300
Db 271 CCACCCGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCT 330
Qy 301 GAAGTTAAGCCTAAATCAGAAGAGAGGGCTCCCTGAAGTTAGAGGATCTACCTACTGTT 360
Db 331 GAAGTTAAGCCTAAATCAGAAGAGAGGGCTCCCTGAAGTTAGAGGATCTACCTACTGTT 390
Qy 361 GAGGCTCTGGAGATCCTCAAGAACCCAGAAATAATGCCACAGGGACAAAGAGGGGAT 420
Db 391 GAGGCTCTGGAGATCCTCAAGAACCCAGAAATAATGCCACAGGGACAAAGAGGGGAT 450
Qy 421 GACCAGAGTCATTGGCGCTATGGAGGCGACCCGCCCTGGCCCCGGGTGTCCCCAGCCTGC 480
Db 451 GACCAGAGTCATTGGCGCTATGGAGGCGACCCGCCCTGGCCCCGGGTGTCCCCAGCCTGC 510
Qy 481 GCGGGCCGCTCCAGTCCCGGCTGATATCCGCCCCCGAGCTGCCCGCTTCTGCCCCGGCC 540
Db 511 GCGGGCCGCTTCCAGTCCCGGCTGATATCCGCCCCCGAGCTGCCCGCTTCTGCCCCGGCC 570
Qy 541 CTGCGCCCGCTGGAACCTCTGGGTTCCAGTCCCGCGCTCCAGAACTCGCGCTGCGC 600
Db 571 CTGCGCCCGCTGGAACCTCTGGGTTCCAGTCCCGCGCTCCAGAACTCGCGCTGCGC 630
Qy 601 AACAAATGGCACAGTGTGCAACTGACCTGCCTCTGGGCTAGAGATGGCTCTGGGTCCC 660
Db 631 AACAAATGGCACAGTGTGCAACTGACCTGCCTCTGGGCTAGAGATGGCTCTGGGTCCC 690
Qy 661 GGGCGGGAGTACCGGGCTCTGCAGTGCATCTGCACTGGGGGGCTGCAGGTCTGTCGGGC 720
Db 691 GGGCGGGAGTACCGGGCTCTGCAGTGCATCTGCACTGGGGGGCTGCAGGTCTGTCGGGC 750
Qy 721 TCGGAGCACACTGTGGAAGGCCACCGTTTCCCTGCCGAGATCCACGTGGTTCACTCAGC 780
Db 751 TCGGAGCACACTGTGGAAGGCCACCGTTTCCCTGCCGAGATCCACGTGGTTCACTCAGC 810
Qy 781 ACCGCCCTTGGCAGAGTTGACGAGCCTTGGGGCGCCCGGAGGCCCTGGCCGTGTGGCC 840
Db 811 ACCGCCCTTGGCAGAGTTGACGAGCCTTGGGGCGCCCGGAGGCCCTGGCCGTGTGGCC 870
Qy 841 GCCTTCTGGAGAGGGCCCGGAAGAAACAGTGCCTATGAGCAGTTGCTGTCTGCTTG 900
Db 871 GCCTTCTGGAGAGGGCCCGGAAGAAACAGTGCCTATGAGCAGTTGCTGTCTGCTTG 930
Qy 901 GAAGAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCCAGGACTGGACATATCTGCACTC 960
Db 931 GAAGAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCCAGGACTGGACATATCTGCACTC 990
Qy 961 CTGCCCTCTGACTTACCGCTACTTCCAATATGAGGGGTCTCTGACTACACCGCCCTGT 1020
Db 991 CTGCCCTCTGACTTACCGCTACTTCCAATATGAGGGGTCTCTGACTACACCGCCCTGT 1050
Qy 1021 GCCCAGGGTGTATCTGGACTGTGTTAAACCAGACAGTGAATGCTGAGTGTCTAAGCAGCTC 1080
Db 1051 GCCCAGGGTGTATCTGGACTGTGTTAAACCAGACAGTGAATGCTGAGTGTCTAAGCAGCTC 1110
Qy 1081 CACACCCCTCTGACACCCCTGTGGGACCTGGTGACTCTCGGTACAGCTGAACCTCCGA 1140
Db 1111 CACACCCCTCTGACACCCCTGTGGGACCTGGTGACTCTCGGTACAGCTGAACCTCCGA 1170
Qy 1141 GCGACGCAGCCTTTGAATGGCGAGTGAATGAGGCCTCTTCCCTGTGGAGTGGACAGC 1200
Db 1171 GCGACGCAGCCTTTGAATGGCGAGTGAATGAGGCCTCTTCCCTGTGGAGTGGACAGC 1230
Qy 1201 AGTCCTCGGGCTGTGAGCCAGTCCAGCTGAATTCCTGCTGCTGCTGCTGCTGCTGCTA 1260
Db 1231 AGTCCTCGGGCTGTGAGCCAGTCCAGCTGAATTCCTGCTGCTGCTGCTGCTGCTGCTA 1290
Qy 1261 GCCCTGGTTTTTGGCCTCCTTTTGTGTGTCACCGGTGCGGTCTTGTGTCAGATGAGA 1320
Db 1291 GCCCTGGTTTTTGGCCTCCTTTTGTGTGTCACCGGTGCGGTCTTGTGTCAGATGAGA 1350

RESULT 8

US-10-172-118-574
; Sequence 574, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-999
; CURRENT APPLICATION NUMBER: US/10/172,118
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/380,770
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 574
; LENGTH: 1552
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NM_001216
; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-574

Query Match 100.0%; Score 1522; DB 13; Length 1552;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACAGTCAGCCGCATGGCTCCCTGTGCCCCAGCCCCCTGGTCCCTCTGTTGATCCCGGCC 60
Db 31 ACAGTCAGCCGCATGGCTCCCTGTGCCCCAGCCCCCTGGTCCCTCTGTTGATCCCGGCC 90
Qy 61 CCTGCTCCAGGCCTCAGTGTGCAACTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
Db 91 CCTGCTCCAGGCCTCAGTGTGCAACTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 150
Qy 121 CCCCAGAGGTTGCCCGGATGAGAGGATTCCCCCTTGGGAGGAGGCTCTTCTTGGGAA 180
Db 151 CCCCAGAGGTTGCCCGGATGAGAGGATTCCCCCTTGGGAGGAGGCTCTTCTTGGGAA 210
Qy 181 GATGACCCACTGGCGAGGAGGATCTGCCAGTGAAGAGGATTCAACCAGAGAGGAGGAT 240
Db 211 GATGACCCACTGGCGAGGAGGATCTGCCAGTGAAGAGGATTCAACCAGAGAGGAGGAT 270
Qy 241 CCACCCGAGAGGAGGATCTACTGGAGAGGAGGATCTACTGGAGAGGAGGATCTACCT 300
Db 271 CCACCCGAGAGGAGGATCTACTGGAGAGGAGGATCTACTGGAGAGGAGGATCTACCT 330
Qy 301 GAAGTTAAGCCTAAATCAGAAGAGAGGGCTCCCTGAAGTTAGAGGATCTACCTACTGTT 360

Db 331 GAAGTTAAGCCTAAATCAGAAGAAAGAGGGCTCCCTGAAGTTAGAGGATCTACCTACTGTT 390

Qy 361 GAGGCTCCTGGAGATCCTCAAGAACCAGAAATAATGCCACAGGACAAAGAAGGGAT 420

Db 391 GAGGCTCCTGGAGATCCTCAAGAACCAGAAATAATGCCACAGGACAAAGAAGGGAT 450

Qy 421 GACCAGAGTCATTGGCGCTATGGAGGCGACCCCGCTGGCCCGGGTGTCCTCCAGCCTGC 480

Db 451 GACCAGAGTCATTGGCGCTATGGAGGCGACCCCGCTGGCCCGGGTGTCCTCCAGCCTGC 510

Qy 481 GCGGGCCGCTTCAGTCCCCGGTGGATATCGCCCCCAGCTCGCCGCTTCTGCCCGGCC 540

Db 511 GCGGGCCGCTTCAGTCCCCGGTGGATATCGCCCCCAGCTCGCCGCTTCTGCCCGGCC 570

Qy 541 CTGCGCCCCCTGGAACCTCCTGGCTTCAGCTCCCGCGCTCCAGAACTGCGCCTGCGC 600

Db 571 CTGCGCCCCCTGGAACCTCCTGGCTTCAGCTCCCGCGCTCCAGAACTGCGCCTGCGC 630

Qy 601 AACAATGGCCACAGTGTGCAACTGACCTGCTCCTGGCTAGAGATGGCTCTGGGTCCC 660

Db 631 AACAATGGCCACAGTGTGCAACTGACCTGCTCCTGGCTAGAGATGGCTCTGGGTCCC 690

Qy 661 GGGCGGAGTACCGGCTCTGCAGTGCATCTGCACTGGGGGCTGCAGGTGCTCGCGGC 720

Db 691 GGGCGGAGTACCGGCTCTGCAGTGCATCTGCACTGGGGGCTGCAGGTGCTCGCGGC 750

Qy 721 TCGGAGCACACTGTGGAAGGCCACCGTTTCCCTGCCAGATCCACGTGTTTCACTCAGC 780

Db 751 TCGGAGCACACTGTGGAAGGCCACCGTTTCCCTGCCAGATCCACGTGTTTCACTCAGC 810

Qy 781 ACCGCCCTTTGCCAGAGTTGACGAGGCCCTTGGGGCGCCCGGAGGCCTGGCGTGTGGCC 840

Db 811 ACCGCCCTTTGCCAGAGTTGACGAGGCCCTTGGGGCGCCCGGAGGCCTGGCGTGTGGCC 870

Qy 841 GCCTTTCTGGAGGAGGCCCGGAAGAAACAGTGCCTATGAGCAGTTGCTGTCTCGCTTG 900

Db 871 GCCTTTCTGGAGGAGGCCCGGAAGAAACAGTGCCTATGAGCAGTTGCTGTCTCGCTTG 930

Qy 901 GAAGAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCCAGGACTGGACATATCTGCATC 960

Db 931 GAAGAAATCGCTGAGGAAGGCTCAGAGACTCAGGTCCCAGGACTGGACATATCTGCATC 990

Qy 961 CTGCCCTCTGACTTCAGCCGCTACTTCCAAATATAGGGGTCTCTGACTACACCGCCCTGT 1020

Db 991 CTGCCCTCTGACTTCAGCCGCTACTTCCAAATATAGGGGTCTCTGACTACACCGCCCTGT 1050

Qy 1021 GCCCAGGTGTATCTGGAAGTGTGTTTAAACCAGACAGTGTGCTGAGTGTCTAAGCAGTCT 1080

Db 1051 GCCCAGGTGTATCTGGAAGTGTGTTTAAACCAGACAGTGTGCTGAGTGTCTAAGCAGTCT 1110

Qy 1081 CACACCTCTCTGACACCCCTGTGGGACCTGGTGACTCTCGGTACAGCTGAACCTCCGA 1140

Db 1111 CACACCTCTCTGACACCCCTGTGGGACCTGGTGACTCTCGGTACAGCTGAACCTCCGA 1170

Qy 1141 GCGACGCAGCCTTTGAATGGCGAGTGAATGAGGCCTCCTTCCCTGCTGGAGTGGACAGC 1200

Db 1171 GCGACGCAGCCTTTGAATGGCGAGTGAATGAGGCCTCCTTCCCTGCTGGAGTGGACAGC 1230

Qy 1201 AGTCTCGGGCTGCTGAGCCAGTCCAGCTGAATTCCTGCTGGCTGCTGGTGACATCCTA 1260

Db 1231 AGTCTCGGGCTGCTGAGCCAGTCCAGCTGAATTCCTGCTGGCTGCTGGTGACATCCTA 1290

Qy 1261 GCCCTGGTTTGTGCTCCTTTTGTGTGCTCACCAGCGTCGCGTTCTTGTGCAGATGAGA 1320

Db 1291 GCCCTGGTTTGTGCTCCTTTTGTGTGCTCACCAGCGTCGCGTTCTTGTGCAGATGAGA 1350

Qy 1321 AGGCAGCACAGAAGGGGAACCAAGGGGGTGTGAGCTACCGCCAGCAGAGGTAGCCGAG 1380

Db 1351 AGGCAGCACAGAAGGGGAACCAAGGGGGTGTGAGCTACCGCCAGCAGAGGTAGCCGAG 1410

Qy 1381 ACTGGAGCCTAGAGGCTGGATCTTGGAGAAATGTGAGAAAGCCAGCAGAGGCATCTGAGGG 1440

Db 1411 ACTGGAGCCTAGAGGCTGGATCTTGGAGAAATGTGAGAAAGCCAGCAGAGGCATCTGAGGG 1470

Qy 1441 GGAGCCGGTAACTGTCTGTCTCTCATTATGCCACTTCTCTTTAACTGCCAAGAAAT 1500

Db 1471 GGAGCCGGTAACTGTCTGTCTCTCATTATGCCACTTCTCTTTAACTGCCAAGAAAT 1530

Qy 1501 TTTTAAATAAATATTTATAAT 1522

Db 1531 TTTTAAATAAATATTTATAAT 1552

RESULT 9

US-10-388-360-291

; Sequence 291, Application US/10388360

; Publication No. US2003022528A1

; GENERAL INFORMATION:

; APPLICANT: GENOMIC HEALTH

; APPLICANT: Baker, Joffre B.

; APPLICANT: Cronin, Maureen T.

; APPLICANT: Kiefer, Michael C.

; APPLICANT: Shak, Steve

; APPLICANT: Walker, Michael Graham

; TITLE OF INVENTION: GENE EXPRESSION PROFILING IN BIOPSIED TUMOR TISSUES

; FILE REFERENCE: 39740-0001US

; CURRENT APPLICATION NUMBER: US/10/388,360

; CURRENT FILING DATE: 2003-03-12

; PRIOR APPLICATION NUMBER: US 60/412,049

; PRIOR FILING DATE: 2002-09-18

; PRIOR APPLICATION NUMBER: US 60/364,890

; PRIOR FILING DATE: 2002-03-13

; NUMBER OF SEQ ID NOS: 384

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 291

; LENGTH: 1552

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-388-360-291

Query Match 100.0%; Score 1522; DB 13; Length 1552;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACAGTCAGCCGATGGCTCCCTGTGCCCCAGCCCCCTGGCTCCTCTGTTGATCCCGGCC 60

Db 31 ACAGTCAGCCGATGGCTCCCTGTGCCCCAGCCCCCTGGCTCCTCTGTTGATCCCGGCC 90

Qy 61 CCTGCTCCAGCCTCACTGTGCAACTGCTGTCTCACTGTCTGTGATGCCTGTCCAT 120

Db 91 CCTGCTCCAGCCTCACTGTGCAACTGCTGTCTCACTGTCTGTGATGCCTGTCCAT 150

Qy 121 CCCCAGAGTTGCCCGGATGCAGGAGGATCCCCCTTGGGAGGAGCTTCTTCTGGGAA 180

Db 151 CCCCAGAGTTGCCCGGATGCAGGAGGATCCCCCTTGGGAGGAGCTTCTTCTGGGAA 210

Qy 181 GATGACCCACTGGGCGAGGAGGATCTGCCAGTGAAGAGGATTCACCCAGAGAGGAGAT 240

Db 211 GATGACCCACTGGGCGAGGAGGATCTGCCAGTGAAGAGGATTCACCCAGAGAGGAGAT 270

Qy 241 CCACCCGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCT 300

Db 271 CCACCCGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCT 330

Qy 301 GAAGTTAAGCCTAAATCAGAAGAGAGGGCTCCCTGAAGTTAGAGGATCTACCTACTGTT 360

Db 331 GAAGTTAAGCCTAAATCAGAAGAGAGGGCTCCCTGAAGTTAGAGGATCTACCTACTGTT 390

Qy 361 GAGGCTCCTGGAGATCCTCAAGAACCCAGAAATAATGCCACAGGACAAAGAAGGGGAT 420

Db 391 GAGGCTCCTGGAGATCCTCAAGAACCCAGAAATAATGCCACAGGACAAAGAAGGGGAT 450

Qy 421 GACCAGAGTCATTGGCGCTATGGAGGCGACCCCGCTGGCCCGGGTGTCCCCAGCCTGC 480

Db 451 GACCAGAGTCATTGGCGCTATGGAGGCGACCCCGCTGGCCCGGGTGTCCCCAGCCTGC 510

||||| 511 GCGGCGCGTTCAGTCCCGTGGATATCGCCCCCAGCTCGCGCCTTCTGCCCGGCC 570
QY 541 CTGCGCCCCCTGGAACCTCTGGGCTTCCAGTCCCGCCGCTCCAGAACTGCGCCTGCGC 600
Db 571 CTGCGCCCCCTGGAACCTCTGGGCTTCCAGTCCCGCCGCTCCAGAACTGCGCCTGCGC 630
QY 601 AACAAATGGCCACAGTGTGCAACTGACCCCTGCCTCTGGGCTAGAGATGGCTCTGGGTCCC 660
Db 631 AACAAATGGCCACAGTGTGCAACTGACCCCTGCCTCTGGGCTAGAGATGGCTCTGGGTCCC 690
QY 661 GGGCGGGAGTACCGGGCTCTGCAGCTGCAATCTGCACCTGGGGGCTGCAGGTCTGTCGGGC 720
Db 691 GGGCGGGAGTACCGGGCTCTGCAGCTGCAATCTGCACCTGGGGGCTGCAGGTCTGTCGGGC 750
QY 721 TCGGAGCACACTGTGGAAGGCCACCGTTTCCCTGCCGAGATCCACGTGGTTCAACCTCAGC 780
Db 751 TCGGAGCACACTGTGGAAGGCCACCGTTTCCCTGCCGAGATCCACGTGGTTCAACCTCAGC 810
QY 781 ACCGCCCTTTCACAGATTGACGAGGCCCTTGGGGCGCCCCGGAGGCCTGGCCGTGTTGGCC 840
Db 811 ACCGCCCTTTCACAGATTGACGAGGCCCTTGGGGCGCCCCGGAGGCCTGGCCGTGTTGGCC 870
QY 841 GCCTTTCTGGAGAGGGCCCCGGAAGAAACAGTGCCTATGAGCAGTTGCTGTCTCGCTTG 900
Db 871 GCCTTTCTGGAGAGGGCCCCGGAAGAAACAGTGCCTATGAGCAGTTGCTGTCTCGCTTG 930
QY 901 GAAGAAATCGTGAGGAAGGCTCAGAGACTCAGGTCCCAGGACTGGACATATCTGCACCTC 960
Db 931 GAAGAAATCGTGAGGAAGGCTCAGAGACTCAGGTCCCAGGACTGGACATATCTGCACCTC 990
QY 961 CTGCCCCTCTGACTTCAGCCGCTACTTCCAATATGAGGGGTCTCTGACTACACCGCCCTGT 1020
Db 991 CTGCCCCTCTGACTTCAGCCGCTACTTCCAATATGAGGGGTCTCTGACTACACCGCCCTGT 1050
QY 1021 GCCCAGGGTGTCACTTGGACTGTGTTTAAACCAGACAGTGATGCTGAGTGCTAAGCAGCTC 1080
Db 1051 GCCCAGGGTGTCACTTGGACTGTGTTTAAACCAGACAGTGATGCTGAGTGCTAAGCAGCTC 1110
QY 1081 CACACCCCTCTTGACACCCCTGTGGGGACCTGGTGACTCTCGGCTACAGCTGAACCTTCGA 1140
Db 1111 CACACCCCTCTTGACACCCCTGTGGGGACCTGGTGACTCTCGGCTACAGCTGAACCTTCGA 1170
QY 1141 GCGACGCAGCCTTTGAATGGGCGAGTGATTGAGGCCCTCCTTCCCTGCTGGAGTGGACAGC 1200
Db 1171 GCGACGCAGCCTTTGAATGGGCGAGTGATTGAGGCCCTCCTTCCCTGCTGGAGTGGACAGC 1230
QY 1201 AGTCCTCGGGCTGTGAGCCAGTCCAGCTGAATTCCTGCCTGGTGTGCTGGTACATCCTA 1260
Db 1231 AGTCCTCGGGCTGTGAGCCAGTCCAGCTGAATTCCTGCCTGGTGTGCTGGTACATCCTA 1290
QY 1261 GCCCTGGTTTTTGCCCTCCTTTTGTCTGCACAGCGTCGCGTTCTTGTGCAGATGAGA 1320
Db 1291 GCCCTGGTTTTTGCCCTCCTTTTGTCTGCACAGCGTCGCGTTCTTGTGCAGATGAGA 1350
QY 1321 AGGCAGCACAGAAAGGGGAACCAAAGGGGGTGTGAGCTACCGCCACGAGAGGTAGCCGAG 1380
Db 1351 AGGCAGCACAGAAAGGGGAACCAAAGGGGGTGTGAGCTACCGCCACGAGAGGTAGCCGAG 1410
QY 1381 ACTGGAGCCTAGAGCCTGGATCTTGGAGAAATGTGAGAAAGCCAGCAGAGGCATCTGAGGG 1440
Db 1411 ACTGGAGCCTAGAGCCTGGATCTTGGAGAAATGTGAGAAAGCCAGCAGAGGCATCTGAGGG 1470
QY 1441 GGAGCCGGTAACGTCTCTGTCTGCTCAATATGCCACTTCCCTTTTAACTGCCAAGAAATT 1500
Db 1471 GGAGCCGGTAACGTCTCTGTCTGCTCAATATGCCACTTCCCTTTTAACTGCCAAGAAATT 1530
QY 1501 TTTTAAATAAATAATTTATAAT 1522
Db 1531 TTTTAAATAAATAATTTATAAT 1552

US-10-465-572-9
; Sequence 9, Application US/10465572
; Publication No. US20030207840A1
; GENERAL INFORMATION:
; APPLICANT: Riggins, Gregory
; APPLICANT: Lal, Anita
; TITLE OF INVENTION: GENES INDUCED BY HYPOXIA
; FILE REFERENCE: 000250.00012
; CURRENT APPLICATION NUMBER: US/10/465,572
; CURRENT FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US/10/201,642
; PRIOR FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: 60/307,600
; PRIOR FILING DATE: 2001-07-26
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 1552
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-465-572-9
Query Match 100.0%; Score 1522; DB 16; Length 1552;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ACAGTCAGCCGCATGGCTCCCTGTGCCCCCAGCCCCCTGGCTCCCTCTGTTGATCCCGGCC 60
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QY 61 CCTGCTCCAGGCCTCACTGTGCAACTGCTGTCTCACTGCTGTTCTGATGCCTGTCCAT 120
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QY 121 CCCCAGAGTTGCCCCGGATGCAGAGGATTTCCCCCTTGGGAGGAGGCTCTTCTGCGGAA 180
Db 151 CCCCAGAGTTGCCCCGGATGCAGAGGATTTCCCCCTTGGGAGGAGGCTCTTCTGCGGAA 210
QY 181 GATGACCCACTGGGCGAGGAGGATCTGCCAGTGAAGAGGATTCACCCAGAGAGGAGAT 240
Db 211 GATGACCCACTGGGCGAGGAGGATCTGCCAGTGAAGAGGATTCACCCAGAGAGGAGAT 270
QY 241 CCACCCGGAGAGGAGGATCTACCTCGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCT 300
Db 271 CCACCCGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCT 330
QY 301 GAAGTTAAGCCTAAATCAGAAAGAGGGGCTCCCTGAAGTTAGAGGATCTACCTACTGTT 360
Db 331 GAAGTTAAGCCTAAATCAGAAAGAGGGGCTCCCTGAAGTTAGAGGATCTACCTACTGTT 390
QY 361 GAGGCTCCTGGAGATCCTCAAGAACCCAGAAATAATGCCACAGGGACAAAGAGGGGAT 420
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QY 481 GCGGGCCGCTTCAGTCCCGGTGGATATCGCCCCCAGTCCGCCCTTCTGCCCGGCC 540
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QY 661 GGGCGGGAGTACCGGGCTCTGCAGCTGCAATCTGCACCTGGGGGCTGCAGGTCTGTCGGGC 720
Db 691 GGGCGGGAGTACCGGGCTCTGCAGCTGCAATCTGCACCTGGGGGCTGCAGGTCTGTCGGGC 750

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QY 781 ACCGCCCTTTGCCAGAGTTGACGAGCCCTTGGGGGCCCGGAGGCTGGCCGTGTGGCC 840
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Db 811 ACCGCCCTTTGCCAGAGTTGACGAGCCCTTGGGGGCCCGGAGGCTGGCCGTGTGGCC 870
|
QY 841 GCCTTTCTGGAGGAGGGCCCGGAAGAAAACAGTGCCTATGAGCAGTTGCTGCTCGCTTG 900
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Db 871 GCCTTTCTGGAGGAGGGCCCGGAAGAAAACAGTGCCTATGAGCAGTTGCTGCTCGCTTG 930
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Db 1531 TTTTAAATAAATATTATAAT 1552
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RESULT 12
US-10-295-027-305
; Sequence 305, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
```

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; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 305
; LENGTH: 1552
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-295-027-305
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Query Match 100.0%; Score 1522; DB 16; Length 1552;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACAGTCAGCCGCATGGCTCCCTGTGCCCCAGCCCTGGCTCCCTCTGTTGATCCCGGCC 60
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Db 31 ACAGTCAGCCGCATGGCTCCCTGTGCCCCAGCCCTGGCTCCCTCTGTTGATCCCGGCC 90
|
QY 61 CCTGCTCCAGGCCCTCACTGTGCAACTGCTGTCTCACTGTCTTCTGATGCCTGTCCAT 120
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Db 91 CCTGCTCCAGGCCCTCACTGTGCAACTGCTGTCTCACTGTCTTCTGATGCCTGTCCAT 150
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|
Db 151 CCCAGAGGTTGCCCGGATGCAGGAGGATTCCCCCTTGGGAGGAGGCTCTTCTGGGAA 210
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QY 181 GATGACCCACTGGCGAGGAGGATCTGCCCCAGTGAAGAGGATTACCCAGAGAGGAGGAT 240
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Db 211 GATGACCCACTGGCGAGGAGGATCTGCCCCAGTGAAGAGGATTACCCAGAGAGGAGGAT 270
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QY 241 CCACCCGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCT 300
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|
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Db 391 GAGGCTCCTGGAGATCCTCAAGAACCCCAAGATATATGCCACAGGGACAAAGAGGGGAT 450
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QY 421 GACCAGAGTCAATTGGCGCTATGGAGGCGACCCGCCCTGGCCCCCGGGTGTCCCCAGCCTGC 480
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Db 451 GACCAGAGTCAATTGGCGCTATGGAGGCGACCCGCCCTGGCCCCCGGGTGTCCCCAGCCTGC 510
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QY 1501 TTTTAAATAAATAATTTATAAT 1522
Db |||||
QY 1531 TTTTAAATAAATAATTTATAAT 1552
Db |||||

RESULT 13
US-10-295-027-1022
; Sequence 1022, Application US/10295027

Publication No. US20030232350A1
GENERAL INFORMATION:
APPLICANT: Afar, Daniel
APPLICANT: Aziz, Natasha
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Gish, Kurt C.
APPLICANT: Glynn, Richard
APPLICANT: Hevezi, Peter A.
APPLICANT: Mack, David H.
APPLICANT: Murray, Richard
APPLICANT: Watson, Susan R.
APPLICANT: Eos Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
FILE REFERENCE: 018501-012500US
CURRENT APPLICATION NUMBER: US/10/295,027
CURRENT FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: US 09/663,733
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: US 60/350,666
PRIOR FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/335,394
PRIOR FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: US 60/332,464
PRIOR FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: US 60/334,393
PRIOR FILING DATE: 2001-11-29
PRIOR APPLICATION NUMBER: US 60/340,376
PRIOR FILING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: US 60/347,211
PRIOR FILING DATE: 2002-01-08
PRIOR APPLICATION NUMBER: US 60/347,349
PRIOR FILING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: US 60/355,250
PRIOR FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: US 60/356,714
PRIOR FILING DATE: 2002-02-13
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1386
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1022
LENGTH: 1552
TYPE: DNA
ORGANISM: Homo sapiens
US-10-295-027-1022

Query Match 100.0%; Score 1522; DB 16; Length 1552;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACAGTCAGCCGATGGCTCCCTGTGCCAGCCCTGGTCCCTCTGTGATCCCGGCC 60
Db |||||
QY 31 ACAGTCAGCCGATGGCTCCCTGTGCCAGCCCTGGTCCCTCTGTGATCCCGGCC 90
Db |||||
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QY 121 CCCAGAGGTTGCCCGGATGCAGGAGGATCCCTTGGGAGGAGGCTCTTCTGGGGA 180
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Db 541 CGCCCCCTGGAACTCTCGGGCTTCAGCTCCCGCGCTCCAGAACTCGGCCTCGGCAAC 600
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Qy 724 GAGCACACTGTGGAAGGCCACCGTTTCCCTGCCAGATCCACGTGTTACCTCAGCAC 783
Db 721 GAGCACACTGTGGAAGGCCACCGTTTCCCTGCCAGATCCACGTGTTACCTCAGCAC 780
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RESULT 15

US-09-783-708-2

; Sequence 2, Application US/09783708

; Patent No. US20020058041A1

; GENERAL INFORMATION:

; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: KIDNEY-SPECIFIC TUMOR VACCINE DIRECTED AGAINST KIDNEY TUMOR ANTIG
; FILE REFERENCE: 306T-897420US
; CURRENT APPLICATION NUMBER: US/09/783,708
; CURRENT FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: 60/182,429
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 60/182,636
; PRIOR FILING DATE: 2000-02-15
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 1833
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Nucleic acid encoding G250-GM-CSF fusion protein with His tag
US-09-783-708-2

Query Match 90.7%; Score 1379.8; DB 9; Length 1833;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1381; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy 136 CGGATGCAGGAGGATTCCCCCTTGGGAGGAGGCTCTTCTGGGGAAGATGACCCACTGGGC 195
Db 559 CGGATGCAGGAGGATTCCCCCTTGGGAGGAGGCTCTTCTGGGGAAGATGACCCACTGGGC 618
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Db 739 TCAGAAAGAAGAGGCTCCCTGAAGTTAGAGGATCTACCTACTGTGAGGCTCCTGGAGAT 798
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Db 799 CCTCAAGAACCCCAAGATAATGCCACAGGACAAAGAGGGGATGACAGAGTCAATTGG 858
Qy 436 CGCTATGGAGGGCAGCCCGCCCTGGCCCGGGTGTCCCCAGCCTCGCGGGCCGCTTCCAG 495
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Qy 496 TCCCCGGTGGATATCCGCCCCCAGCTCGCCGCTTCTGCCCGGCCCTGCGCCCCCTGGAA 555
Db 919 TCCCCGGTGGATATCCGCCCCCAGCTCGCCGCTTCTGCCCGGCCCTGCGCCCCCTGGAA 978
Qy 556 CTCCTGGGCTTCCAGTCCCGCCGCTCCAGAACTGCGCCTGCGCAACAATGGCCACAGT 615
Db 979 CTCCTGGGCTTCCAGTCCCGCCGCTCCAGAACTGCGCCTGCGCAACAATGGCCACAGT 1038
Qy 616 GTGCAACTGACCCCTGCTCTGGGCTAGAGTGGCTCTGGGTCCCGGGGGAGTACCGG 675
Db 1039 GTGCAACTGACCCCTGCTCTGGGCTAGAGTGGCTCTGGGTCCCGGGGGAGTACCGG 1098
Qy 676 GCTCTGCAGCTGCATCTGCACTGGGGGCTGCAGGTCGTCCGGGCTCGAGACACACTGTG 735
Db 1099 GCTCTGCAGCTGCATCTGCACTGGGGGCTGCAGGTCGTCCGGGCTCGAGACACACTGTG 1158
Qy 736 GAAGGCCACCGTTTCCCTGCCGAGATCCACGTGTTTACCTCAGCACCGCCTTTGCCAGA 795
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Db	1159	GAAGGCCACCGTTTCCTGCCGAGATCCACGTGTTACCTCAGCACCGCCTTTGCCAGA	1218
QY	796	GTTGACGAGGCCTTGGGGCGCCCGGAGGCTGGCCGTTGTCGCGCCTTCTCTGGAGAG	855
Db	1219	GTTGACGAGGCCTTGGGGCGCCCGGAGGCTGGCCGTTGTCGCGCCTTCTCTGGAGAG	1278
QY	856	GGCCCGGAAGAAACAGTGCCTATGAGCAGTTGCTGTCTCGCTTGAAGAAATCGCTGAG	915
Db	1279	GGCCCGGAAGAAACAGTGCCTATGAGCAGTTGCTGTCTCGCTTGAAGAAATCGCTGAG	1338
QY	916	GAAGGCTCAGAGACTCAGGTCCCAGGACTGACATATCTGCACTCCTGCCCTCTGACTTC	975
Db	1339	GAAGGCTCAGAGACTCAGGTCCCAGGACTGACATATCTGCACTCCTGCCCTCTGACTTC	1398
QY	976	AGCCGCTACTTCCAAATATGAGGGGTCTCTGACTACACCGCCCTGTGCCCCAGGGTGTCATC	1035
Db	1399	AGCCGCTACTTCCAAATATGAGGGGTCTCTGACTACACCGCCCTGTGCCCCAGGGTGTCATC	1458
QY	1036	TGGACTGTGTTTAAACAGACAGTGATGTGAGTGCTAAGCAGTCCACACCCCTCTCTGAC	1095
Db	1459	TGGACTGTGTTTAAACAGACAGTGATGTGAGTGCTAAGCAGTCCACACCCCTCTCTGAC	1518
QY	1096	ACCTGTGGGACCTGGTGACTCTCGGCTACAGCTGAACCTCCGAGCGACGCGCCTTTG	1155
Db	1519	ACCTGTGGGACCTGGTGACTCTCGGCTACAGCTGAACCTCCGAGCGACGCGCCTTTG	1578
QY	1156	AATGGCGAGTGATTGAGGCCTCCTTCCCTGCTGGAGTGGACAGCAGTCCCTCGGGCTGCT	1215
Db	1579	AATGGCGAGTGATTGAGGCCTCCTTCCCTGCTGGAGTGGACAGCAGTCCCTCGGGCTGCT	1638
QY	1216	GAGCCAGTCCAGCTGAATTCTGCTGGCTGCTGGTGACATCTAGCCCTGGTTTTTTGGC	1275
Db	1639	GAGCCAGTCCAGCTGAATTCTGCTGGCTGCTGGTGACATCTAGCCCTGGTTTTTTGGC	1698
QY	1276	CTCCTTTTGTGTCACACGCGTCGCGTTCTTGTGCAGATGAGAAGGCAGCACAGAAGG	1335
Db	1699	CTCCTTTTGTGTCACACGCGTCGCGTTCTTGTGCAGATGAGAAGGCAGCACAGAAGG	1758
QY	1336	GGAACCAAGGGGTGTGAGCTACCGCCAGCAGAGGTAGCCGAGACTGGAGCCTAGAGG	1395
Db	1759	GGAACCAAGGGGTGTGAGCTACCGCCAGCAGAGGTAGCCGAGACTGGAGCCTAGATG	1818
QY	1396	CTG 1398	
Db	1819	GTG 1821	